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Sequence:
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Listing first 45 summaries
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                                                                                                                                                                                                        Score
                                                                                                                              551
74.5
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Copyright (c) 1993 - 2003 Compugen Ltd.
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AAW31738
AAB10456
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ABB96121
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                                                                                                                                                                                                   Description
                                                                                            Macadamia integrif
S. pastorianus mut
Cynomologous monke
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PI Goulter KC, Green JL, Harrison SJ, Manners JM, XX	PA (RETR-) COOP RES CENT TROPICAL PLANT PATHOLOGY.	PR 31-JAN-1996; 96AU-0007802.	PF 31-JAN-1997; 97WO-AU00052.	PD 07-AUG-1997. XX	PN W09728185-A1. XX	Peptide 27102	Peptide	OS Macadamia integrifolia.		DE Macadamia integrifolia antimicrobial protein 1.	DT 27-MAR-1998 (first entry) XX	AAW31738;	RESULT 1 AAW31738
JM, Marcus JP;	•								ngus; bacterium	•			

70.5 70.5 70.5

12.9 12.9 12.8 12.8 12.8 12.5 12.5

1280 1283 267 267 267 267 267 138

Cynomologous monke Human testicular a Human reproductive Novel signal trans

Archaebacterium AE Propionibacterium Dog P-glycoprotein

AAW34998 AAU50762

Goulter F	TR-)	31-JAN-19	31-JAN-19	07-AUG-19	WO9728185	Key Peptide Peptide	Macadamia	Antimicro fungi; ba	Macadamia	27-MAR-19	AAW31738	SULT 1 W31738 AAW31738		6	 0.0	. 6	60	n 01	8 0 ~	, 0	4.10		6 B	60	 	90	25	љ . "		, O	. 0. 0	7 68.	68.	4.1	9 6) L
KC, Green JL, Harrison SJ	PRE	996; 96AU-0007802.	997; 97WO-AU00052.	997.	5-A1.	Location/Qualifiers 126 /label= sig_peptide 27102 /label= mat_peptide	a integ	obial protein 1; growth inhi	a integrifolia antimicrobi	1998 (first entry)	÷	standard; Protein; 102 AA.	ALI	8 12.3 1280 23	8 12.3 1280 23 8 12.3 1280 23	8 12.3 1280 23	8 12.3 1280 23	8 12.3 1280 23	8 12.3 1280 23 8 12.3 1280 23	8 12.3 1280 23	8 12.3 1280 23 8 12.3 1280 23	8 12.3 1280 23	8 12.3 1280 23 8 12.3 1280 23	8 12.3 1280 22	8 12.3 1280 22 8 12.3 1280 22	8 12.3 1280 22	58 12.3 1280 21 AAYS8186	8 12.3 1280 19 8 12.3 1280 19	8 12.3 1280 18	8 12.3 1280 14	8 12.3 1280 11	5 12.4 1280 19	5 12.4 1280 19	9 12.5 1281 22	9 12.5 1281 22	9 12.5 1280 22
J, Manners JM, Marcus	NT PATHOLOGY.					0 0 O		bition; fungus;	al protein 1.				ALIGNMENTS	976	974 975	973	972	970	969	967	965	964	211	306	066	347	186	997	073	297	868	000	1998	309	308	1304
cus JP;								bacterium;							n P-9	n P-91	Human P-gp mutant,	n P-9	P-9	n P-g	Human P-gp mutant, Human P-gp mutant.	Human wild type P-	MDR	φ-q	Human P-glycoprote	1 G	Human wild-type mu	Wild-type human P	Human multidrug re	encoded	oded oded	Human	coprote ll singl	coprote	raoor P-gl	coprote

Length 486;

DB 21;

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Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mutant hexokinase, useful for the detection of creatinine kinase and glucose, comprises a deletion, addition or insertion in the wild-type amino acid sequence -
                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                          1 MASTKLFFSVITVMMLIAMASEMVNGSAFTVWSGPGCNNRAERYSKCGCSAIHQKGGYDF 60
                                                                                                                                                                                                                                                                                                                      1 MASIKLFFSVIIVMMLIAMASEMVNGSAFIVWSGFGCNNRAERYSKCGCSAIHQKGGYDF 60
                                                                                                                  The present sequence is Macadamia integrifolia antimicrobial protein 1, which exerts inhibitory activity on the growth of fungiand bacteria. It can be used for the control of pathogens in plants
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Hexokinase; mutant; creatinine kinase detection; glucose detection.
                                                          inhibiting the growth of fungi and bacteria in plants and animals
                                           anti-microbial protein from Macadamia integrifolia - active
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                                                                                                                                                                                                                                Length 102;
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                                                                                                                                                                                                                                                                                                                                                         SYTGQTAALYNQAGCSGVAHTRFGSSARACNPFGWKSIFIQC 102
                                                                                                                                                                                                                                                                                                                                                                          100.0%; Score 551; DB 18;
100.0%; Pred. No. 1.5e-54;
iive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               pastorianus mutant hexokinase protein.
                                                                                          Claim 1; Pages 23-24; 38pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAB10456 standard; Protein; 486
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                                                                                                                                                                                                                                                  Best Local Similarity 100.
Matches 102, Conservative
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WPI, 1997-448317/41
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                   N-PSDB; AAT88851
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Novel isolated nucleic acid encoding cynomologous monkey P-glycoprotein (PGP) and homologous PGP polypeptides are useful for predicting bioavailability of compound and increasing PGP transporter activity in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Cynomologous monkey; P-glycoprotein; PGP; multidrug transporter; MDR1;
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                                                                                                                                                                                      369 FGINTTVQERKLIRRLSELIGA------RAARLSVCGIAAVCOKRGYK---TG 412
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                                                                                                                               FSVITVMM---LIAMASEMVNGSAFTVWSGPGCNNRAERYSKCGCSAIHQKGGYDFSYTG 64
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                                                                                                                                                                                                                                                                                                      413 HIAA-----DGSVYNRYPGFKEKAANALKDIYGW 441
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Cynomologous monkey P-glycoprotein variant 1.
                                                                                                                                                                                                                                                   OTAALYNOAGCSGVAHTRF-GSSARACNP----FGW 95
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25.5%; Pred. No. 42;
..ive 12; Mismatches
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               13.5%; Score 74.5; 29.2%; Pred. No. 5.
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Query Match
Best Local Similarity 29.29
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                                                                                                                                           This invention relates to a polynucleotide sequence encoding a cynomologous monkey P-glycoprotein (PGP), and an allelic variant of the PGP protein. PGP, also known as multidrug transporter, MDR1 is a member of the ABC transporter superfamily. The enzyme serves as an efflux pump exporting small molecules across the cell membrane. The invention includes a cynomologous monkey (Macaca fascicularis) PGP coding sequence and protein, and also that of an allelic variant. The PGP polynucleotide sequence is useful for increasing PGP transporter activity in a cell. Antisense sequences of the CDNA are useful for inhibiting PGP transport activity in a mammalian cell. They may also be used for increasing the cynomologous monkey P-glycoprotein variant 2. The protein has an additional 3 amino acids when compared to PGP variant 1 (AABB1065).
                                                                                                                        Sequence
                                                                                                                                                                                                                                                                                                                                                                                                 Novel isolated nucleic acid encoding cynomologous monkey P-glycoprotein (PGP) and homologous PGP polypeptides are useful for predicting bioavailability of compound and increasing PGP transporter activity in
                                                                                                                                                                                                                                                                                                                                                           Claim 9; Page 65-68; 84pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   N-PSDB;
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12-OCT-1999;
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Misc-difference 93..95
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (GENT-) GENTEST CORP.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 28-SEP-2000; 2000WO-US26592
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       25-JUN-2001
337 VFFSVLIGAFSVGQASPSIEAFANARGAAFEIFKIIDNKPSIDSYSKSGHKPDNIKGNLE 396
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           394
                                                                             Local
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                           6 LFFSVITVMMLIAMASEMV-----NGSAFTVWSGPGCNNRAERYSKCGCSAIHOKGGYD 59
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DB; AAF86128.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ----FSY-----
                                                                           Similarity
                                                                                                                     1283 AA;
                                                              Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Steimel-Crespi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     monkey P-glycoprotein variant
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      99US-0156921.
99US-0158818.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /note= "An additional 3 amino acids are
to PGP variant AAB81064"
                                                                          12.9%;
                                                            12;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Ğ,
                                                                        Score 71; DB 22;
Pred. No. 42;
                                                          Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Crespi CL;
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                                                          33;
                                                                                     Length 1283;
                                                          Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   present compared
                                                          28;
                                                       Gaps
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ABB96121
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     01-SEP-2000;
01-SEP-2000;
01-SEP-2000;
01-SEP-2000;
05-SEP-2000;
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06-SEP-2000;
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18 - AUG - 2000;
22 - AUG - 2000;
22 - AUG - 2000;
22 - AUG - 2000;
23 - AUG - 2000;
30 - AUG - 2000;
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14-AUG-2000;
14-AUG-2000;
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17-MAR-2000;
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14-AUG-
                                                                                                                                                                                                                                                                                                                        07-JUN-2000;
28-JUN-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Human; testicular antigen; testes; cancer; metastasis; immune disorder; reproductive system disorder; urinary system disorder; gene thorapy; cardiovascular disorder; respiratory disorder; neurological disorder; gastrointestinal disease; infection; cytostatic.
                                                                                                                                                               14-AUG-2000
                                                                                                                                                                                                                                      26-JUL-2000;
14-AUG-2000;
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26-JUL-2000;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Human testicular antigen SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 21-JUN-2002 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ABB96121 standard; Protein; 267 AA
                                                                                                                                                                                                                                                                                                                                           19-MAY-2000;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     397
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             2000US-0229344.
2000US-0229345.
2000US-0229509.
2000US-0229513.
2000US-0230437.
                                                                             2000US-0227182.
2000US-0227009.
2000US-0228924.
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2000US-0225758.
2000US-0225759.
2000US-0226279.
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2000US-0205515.
2000US-0209467.
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2000US-0226868.
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2000US-0217496.
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2000US-0236370.
2000US-0236802.
2000US-0237037.
2000US-0237038.
2000US-0237039.
2000US-0237049.
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2000US-0240960.
2000US-0241221.
                                  2000US-0232081.
2000US-0231968.
2000US-0232397.
                                                                                              14-SEP-2000; 2000US-0233065.
21-SEP-2000; 2000US-023423.
21-SEP-2000; 2000US-02349974.
25-SEP-2000; 2000US-0234998.
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27-SEP-2000; 2000US-0235834.
27-SEP-2000; 2000US-0235836.
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29-SEP-2000; 2000US-0236367.
29-SEP-2000; 2000US-0236368.
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2000US-0246476.
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                     2000US-0231414.
2000US-0232080.
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                                                       2000US-0232398
                                                                    2000US-0232400
                                                                           2000US-0232401
08-SEP-2000;
08-SEP-2000;
08-SEP-2000;
08-SEP-2000;
08-SEP-2000;
08-SEP-2000;
12-SEP-2000;
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Human; reproductive system related antigen; reproductive system disorder;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gapa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          28 AFTVWSGPGCNNRAERYSKCGCSAIHOKGGYDFSYTGQTAALYNQAGCSGVAHTRFGSSA 87
                                                                                                                                                                                                                                                                                                                                         Nucleic acids encoding 973 human testicular antigen polypeptides, useful for preventing, diagnosing and/or treating testicular cancer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                5,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   12.8%; Score 70.5; DB 22; Length 267; 27.0%; Pred. No. 7.9; tive 13; Mismatches 36; Indels 5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Human reproductive system related antigen SEQ ID NO: 4089.
                                                                                                                                                                                                                                                                                                                                                                                     Claim 11; SEQ ID NO 1505; 766pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAM95431 standard; Protein; 267 AA
                                                                                                                                                                                                                                                                                       Rosen CA, Barash SC, Ruben SM;
                                    17-NOV-2000; 2000US-0249299.
17-NOV-2000; 2000US-0249300.
01-DEC-2000; 2000US-0250160.
01-DEC-2000; 2000US-0250391.
05-DEC-2000; 2000US-0251030.
05-DEC-2000; 2000US-0251988.
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2000US-0251989.
2000US-0251990.
2000US-0254097.
                                                                                                                                                                                                                                                            (HUMA-) HUMAN GENOME SCI INC
                                                                                                                                                2000US-0251856.
2000US-0251868.
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05-JAN-2001; 2001US-0259678.
          17-NOV-2000; 2000US-0249265.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               88 ---RACNPFGWKSI 98
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Matches 20; Conserval
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    cancer; gene therapy
                                                                                                                                                                                                                                                                                                                 WPI; 2001-483232/52
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Seguence 267 AA;
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17-JAN-2001; 2001WO-US01339.

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1-JAN-2000
04-FEB-2000
24-FEB-2000
12-MAR-2000
16-MAR-2000
17-MAR-2000
19-MAY-2000
07-JUN-2000
28-JUN-2000
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21-SEP-2000
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21-SEP-2000
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07-JUL-2000

11-JUL-2000

11-JUL-2000

11-JUL-2000

14-JUL-2000

26-JUL-2000

14-AUG-2000

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14-AUG-2000

14-AUG-2000
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14-AUG-
14-AUG-
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2000US-0179065.
2000US-0184664.
2000US-0184664.
2000US-019874.
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2000US-0219877.
2000US-0214886.
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2000US-0216887.
2000US-0216887.
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2000US-0231414.
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2000US-02336367.
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2000US-0236369.
2000US-0236369.
  02-OCT-2000

02-OCT-2000

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02-OCT-2000

13-OCT-2000

20-OCT-2000

20-OCT-2000

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20-OCT-2000

20-OCT-2000

01-NOV-2000

08-NOV-2000

01-NOV-2000

17-NOV-2000

17-NO
                           WPI; 2001-465570/50.
N-PSDB; AAL01401.
                                                                 Rosen
  Isolated
                                                                                         (HUMA-)
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                                                                                                                   HUMAN
  nucleic acid
                                                                Barash
                                                                                                                  2000US-0244960

2000US-0241785

2000US-0241786

2000US-0241809

2000US-0244617

2000US-0244617

2000US-0244477

2000US-0246477

2000US-0246477

2000US-0246477

2000US-0246523

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2000US-0237037.
2000US-0237038.
2000US-0237039.
2000US-0237039.
2000US-0237040.
2000US-0239935.
                                                                                          GENOME
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S-0237039.
S-0237040.
S-0239935.
S-0239937.
S-0240960.
                                                                                          SCI
molecule encoding a reproductive system antigen
                                                                 Ruben
                                                                 NS.
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                                       The present invention provides the protein and coding sequences of a number of human reproductive system related antigens. These can be used in the prevention and treatment of reproductive system disorders, including cancer. The present sequence is a protein of the invention.
                                                                                                                                                                Gaps
                                                                                                                                                    28 AFTVWSGPGCNNRAERYSKCGCSAIHQKGGYDFSYTGQTAALYNQAGCSGVAHTRFGSSA 87
 is used in preventing, treating or ameliorating a medical condition
                                                                                                                                 2;
                                                                                                            . Match 12.8%; Score 70.5; DB 22; Length 267; Local Similarity 27.0%; Pred. No. 7.9; es 20; Conservative 13; Mismatches 36; Indels 5,
                   Claim 11; SEQ ID NO 4089; 1297pp + Sequence Listing; English
                                                                                                                                                                                                                                                                                                                            Novel signal transduction pathway protein, Seg ID 1164.
                                                                                                                                                                                                                                                                AAU17599 standard; Protein; 267 AA.
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24-FEB-2000; 2000US-0180628.
24-FEB-2000; 2000US-018664.
02-MAR-2000; 2000US-0189874.
17-MAR-2000; 2000US-0199076.
18-APR-2000; 2000US-0199076.
18-APR-2000; 2000US-0199076.
18-APR-2000; 2000US-029967.
28-JUN-2000; 2000US-021886.
30-JUN-2000; 2000US-021681.
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2000US-0220964.
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                                                                                         Sequence
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AAU17599
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2000US-0241826.
2000US-0244617.
2000US-0246474.
2000US-0246475.
2000US-0246476.
2000US-02464776.
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2000US-0231242,
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05-SEP-2000;
06-SEP-2000;
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08-NOV-2000;
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(HUMA-) HUMAN GENOME SCI INC.
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                                                                                                 Barash SC,
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2000US-0249297.
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2000US-0249209.
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N-PSDB; AAS27516.

Novel polypeptides useful for diagnosing, treating, preventing and/or prognosing disorders related to the proteins, including cancers, immundisorders and neuronal disorders -

SEQ ID No 1164; 880pp; English

CC The invention relates to novel isolated polypeptides (I), and CC polynucleotides (II), (II) and the antibody to (I) are useful for CC disgnosing, preventing and treating diseases including immune system CC disorders (e.g. congenital and acquired immunodeficiencies, autoimmune CC transplant rejections and graft versus host disease, infectious diseases (e.g. hepatitis C), bleeding disorders, haemoglobin abnormalities and CC other blood-related disorders (sickle cell anaemia), myeloproliferative CC disorders, primary haematopoietic disorders, hyperproliferative CC disorders (e.g. Gaucher's disease and cancer), neurodegenerative CC disorders (e.g. Alzheimer's disease, Parkinson's disease), chromosomal CC abnormalities (lown syndrome), ischaemic injury (e.g. stroke), renal CC disorders (e.g. glomerulonephittis), cardiovascular disorders, in conditions (e.g. glomerulonephittis), cardiovascular disorders, in conditions and cell proliferation, endocrine disorders, (e.g. arthythmia), respiratory disorders, dermatological disorders (e.g. arthythmia), respiratory disorders, dermatological disorders (e.g. and ison's disease), renarian, endocrine disorders (e.g. arthythmia), respiratory disorders, dermatological disorders (e.g. and ison's disease), renarian, endocrine disorders (e.g. and ison's disease). Addison's disease), reproductive system disorders, gastrointestinal

AAW34998 Ś 밁 뭐 ននននន Query Match Best Local S Matches 20 produced from native cells or from recombinant host cells, especially prokaryotic host cells transformed with a plasmid or virus-derived vector including the endoglucanase DNA (see AAT94206) 24 Endoglucanases (see AAW34986-W35008) are claimed. They can be used to degrade cellulose for the conversion of plant biomass into fuels and chemicals, for use in detergents, textiles, animal feed, waste treatment, and in the fruit juice and brewing industries for (Clone 63GP1), a hydrothermal vent isolate. The endoglucanase is capable of degrading carboxymethylcellulose and of hydrolysing the beta-1,4-glycosidic bonds in cellulose. It has homology to another endoglucanase (see AAW34985) of archaebacterium AEPIIIa. It can be This the clarification and extraction of Claim 1; Fig lN; 164pp; English. beta-1,4-glycosidic bonds in cellulose Endoglucanase(s), useful to degrade N-PSDB; AAT94206. as stimulators of B-cell responsiveness to pathogens, activators of T-cells, to induce higher affinity antibodies, and as a means to induce tumour proliferation in pathologies e.g. acquired immune deficiency syndrome (AIDS). AAU17059-AAU17683 represent novel signal transduction WPI; 1998-018435/02 27-NOV-1997. Archaebacterium isolate AEPPII1a (Clone 63GP1). biomass; beta-1,4-glycosidic bond; hydrolysis; thermostable enzyme; thermophilic; glycosidase. Lam DE, 22-MAY-1996; 22-MAY-1997; Endoglucanase; cellulase; carboxymethylcellulose; cellulose; Archaebacterium AEPIIla endoglucanase. 21-MAY-1998 AAW34998; AAW34998 standard; pathway protein, amino acid sequences of the invention. disorder (inflammatory disorders), liver disorders (cirrhosis), (RECO-) 146 204 FGGSSSGSSGFKSV 217 88 28 AFTVWSGPGCNNRAERYSKCGCSAIHQKGGYDFSYTGQTAALYNQAGCSGVAHTRFGSSA 87 protein comprises an endoglucanase of archaebacterium AEPIIIa ne 63GP1), a hydrothermal vent isolate. The endoglucanase is SFEFWDSPFNSDRGGRGH--GLRGAFSAGFGEFPAFMEAFSSFNMLGCSGGSHTTFSSTS 203 ---RACNPFGWKSI RECOMBINANT BIOCATALYSIS INC. Similarity Mathur EJ; Conservative (first entry) 97WO-US08793. 96US-0651572 preferably form archael bacterium, AEPII la carboxymethylcellulose and hydrolyse of Protein; 524 12.8%; 13; Score Pred. Mismatches 70.5; DI BB 36; 22; saccharification; Length 5 Gaps

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    polypeptides. The proteins and their associated DNA sequences are used the treatment, prevention and diagnosis of medical conditions caused by the across. The disorders include SAPHO syndrome (synovitis, cane by pustulosis, hypertosis and osteomyelitis), uveitis and endophthalmitis. P. across is also involved in infections of bone, joints and the central nervous system, however it is particularly involved in the inflammatory presence or absence of P. across in a patient comprises contacting the presence or absence of P. across in a patient comprises contacting a sample with a binding agent that binds to the proteins of the invention and determining the amount of bound protein in the sample. The polypeptides may be used as antigens in the production of antibodies appecific for P. across proteins. These antibodies can be used to downregulate expression and activity of P. across polypeptides and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SAPHO syndrome: synovitis; acne; pustulosis; hypertosis; osteomyelitis; uveitis; endophthalmitis; bone; joint; central nervous system; ELISA; inflammatory lesion; acne vulgaris; enzyme linked immunosorbent assay;
                                                                                                                                                                             123 IPEWYEAGISAIWIPPASKGMSGGYSMGYDPYDFFDLGE----YNO---KGTIETRFGSK 175
                                                                                                                                                                                                                                                                     41 AERYSKCGCSAI-----HQKGG-----YDFSYTGQTAALYNQAGCSGVAHTRFGSS 86
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Propionibacterium acnes polypeptides and nucleic acids useful for vaccinating against and diagnosing infections, especially useful
                                                                   43;
   DB 19; Length 524;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Bhatia A;
                                                               37; Indels
                                                                                                                                  3 STKLFFSV-ITVMMLIAMA-----SEMVNGSAFT---VWSGPG---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Propionibacterium acnes immunogenic protein #11658.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              dermatological; osteopathic; neuroprotectant.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Example 1; SEQ ID No 11957; 1069pp; English.
12.8%; Score 70.5; Dl
26.4%; Pred. No. 17;
:ive 12; Mismatches
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02-JUN-2000; 2000US-208841P.
07-JUL-2000; 2000US-216747P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        20-APR-2001; 2001WO-US12865.
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J, Zhang Y,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (first entry)
                                                                      33; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Propionibacterium acnes.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WPI; 2001-616774/71.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (CORI-) CORIXA CORP.
                                      Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      176 QELIN 180
                                                                                                                                                                                                                                                                                                                                                                                                                   87 ARACN 91
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       Query Match
                                                                          Matches
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AAUS0762
ID AAUS
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therefore treat P. acnes infections. The antibodies may also be used as diagnostic agents for determining P. acnes presence, for example, by enzyme linked immunosorbent assay (BLISA).

Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Novel isolated nucleic acid encoding cynomologous monkey P-glycoprotein (PGP) and homologous PGP polypeptides are useful for predicting bioavailability of compound and increasing PGP transporter activity in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Cynomologous monkey; P-glycoprotein; PGP; multidrug transporter; MDR1;
                                                                                                                                                                                                                                             14 MMLIAMASEMVNGSAFTVW-SGPGCNNRAERYSKCGCSAIHQKGGYDFSYTGQTAALYNQ 72
                                                                                                                                                                                                                                                                                53 LMLIRLPRESVQ-----WPSGPASIFRA---SCGTST-----TASTSAAW-V 90
                                                                                                                                                                                                          30,
                                                                                                                                                                    12.5%; Score 69; DB 22; Length 138; 31.5%; Pred. No. 5.4; rive 8; Mismatches 25; Indels 3
                                                                                                at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Crespi CL;
                                                                                                                                                                                                                                                                                                                                                         91 GSCSRIEHTAGAAASSPRISSRLASP-GWKSI 121
                                                                                                                                                                                                                                                                                                                      98
                                                                                                                                                                                                                                                                                                                      73 AGCSGVAHTRFGS-----SARACNPFGWKSI
                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAB81068 standard; Protein; 1280 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Claim 8; Page 73-76; 84pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Steimel-Crespi DT,
                                                                                                                                                                                       Best Local Similarity 31.5%;
Matches 29; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              log P-glycoprotein SEQ ID 7.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    28-SEP-2000; 2000WO-US26592.
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99US-0158818
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (first entry)
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                                                                                                                                     138 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        efflux pump; dog
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                                                                                                                                       Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAB81068;
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1280 AA;

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            Query Match
Best Local (
Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local
                                                                                                                                                             The invention relates to dog P-glycoprotein (PGP) also referred as multidrug transporter (MDR1) and nucleic acids encoding them. The invention also includes fragments and biologically functional variants of dog P-glycoprotein. PGP and their nucleic acids are useful for determining the bioavailability of drugs and for screening PGP inhibitors. They are useful for the diagnosis and treatment of conditions characterised by PGP activity, by reducing or increasing PGP activity in a cell. PGP nucleic acids are useful as antisense oligonucleotides, to induce a PGP (knockout phenotype. They are used to prepare a non-human transgenic animal, which are valuable as genetic models for
                                                                                                 The present sequence is dog P-glycoprotein (PGP). The PGP enzyme functions as an efflux pump exporting small molecules across the cell membrane. This enzyme is a member of the ABC
                                                                                                                                                   human diseases.
                                                                                                                                                                                                                                                                                                                                                                     Example 2; Page 72-75; 111pp; English
                                                                                                                                                                                                                                                                                                                                                                                                               New dog P-glycoproteins (PGP) and their encoding for determining the bioavailability of drugs and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WPI; 2001-235373/24.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Stocker PJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            28-SEP-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          05-APR-2001.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Dog; P-glycoprotein; PGP; multidrug transporter; MDR1; drug bioavailability; transgenic animal; genetic model
                                                                                                                                                                                                                                                                                                                                                                                                       PGP inhibitors
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         28-SEP-2000; 2000WO-US26767.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Dog P-glycoprotein (PGP)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               13-JUN-2001
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAE00304 standard; Protein; 1280 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    395 FKNVHFSYPSRKEVKILKGLNLKVQSGQTVALVGNSGC 432
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           6 LFFSVITVMMLIAMASEMV-----NGSAFTVWSGPGCNNRAERYSKCGCSAIHQKGGYD 59
L Similarity
25; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAD03489
                                                          1280 AA;
                                                                                       family.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             12.5%;
           12.5%; Score 69; DB 25.5%; Pred. No. 70;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 69; DB
Pred. No. 70;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Crespi CL,
                        DB 22; Length 1280;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Reif TC,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 1280;
                                                                                                                                                                                                                                                                                                                                                                                                                nucleic acids, useful for screening for dog
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Patten
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Conservative

12;

Mismatches

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28;

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336 VFFSVLIGAFSIGQASPSIEAFANARGAAYEIFKIIDNKPSIDSYSKSGHKPDNIKGNLE 395

6 LFFSVITVMMLIAMASEMV-----NGSAFTVWSGPGCNNRAERYSKCGCSAIHQKGGYD 59

Matches

25

Conservative

12;

Mismatches

33;

Indels 28;

Gaps

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                        Query Match
                                                                                                                                                                                                                           The invention relates to dog P-glycoprotein (PGP) also referred as multidrug transporter (MDR1) and nucleic acids encoding them. The invention also includes fragments and biologically functional variants of dog P-glycoprotein. PGP and their nucleic acids are useful for determining the bioavailability of drugs and for screening PGP inhibitors. They are useful for the diagnosis and treatment of conditions characterised by PGP activity, by reducing or increasing PGP activity in a cell. PGP nucleic acids are useful as antisense oligonucleotides, to induce a PGP (knockout, phenotype. They are used to propare a non-human PGP).
                                                                                                    The present sequence is dog P-glycoprotein (PGP) also referred as genotype C protein. The PGP enzyme functions as an efflux pump exporting small molecules across the cell membrane. This enzyme is a member of the ABC transporter family.
                                                                   Sequence
                                                                                                                                                                                                  numan
                                                                                                                                                                                                                transgenic animal, which are valuable as genetic models for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Claim 17; Page 64-66; 111pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            New dog P-glycoproteins (PGP) and their encoding nucleic acids, useful for determining the bioavailability of drugs and for screening for dog
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WPI; 2001-235373/24.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   28-SEP-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           28-SEP-2000; 2000WO-US26767.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Dog (PGP) P-glycoprotein (genotype C) #1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAE00303;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAE00303 standard; Protein; 1281 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (GENT-) GENTEST CORP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     335 VFFSVLIGAFSIGQASPSIEAFANARGAAYEIFKIIDNKPSIDSYSKSGHKPDNIKGNLE 394
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    395 FKNVHFSYPSRKEVKILKGLNLKVQSGQTVALVGNSGC 432
    Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   60 -----FSY-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             6 LFFSVITVMMLIAMASEMV-----NGSAFTVWSGPGCNNRAERYSKCGCSAIHQKGGYD 59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            P-glycoprotein; PGP; multidrug transporter; bioavailability; transgenic animal; genetic
                                                                                                                                                                                                diseases.
    Similarity
                                                                   1281 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (first entry)
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12.5%;
Score 69;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               -TGOTAALYNQAGC
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70;
                      22;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Reif TC,
                      Length 1281;
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336 VFFSVLIGAFSIGQASPSIEAFANARGAAYEIFKIIDNKPSIDSYSKSGHKPDNIKGNLE 395

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New dog P-glycoproteins (PGP) and their encoding nucleic acids, useful for determining the bioavailability of drugs and for screening for dog
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          The invention relates to dog P-glycoprotein (PGP) also referred as multidrug transporter (MDR1) and nucleic acids encoding them. The invention also includes fragments and biologically functional variants of dog P-glycoprotein. PGP and their nucleic acids are useful for determining the bioavailability of drugs and for screening PGP inhibitors. They are useful for the diagnosis and treatment of conditions characterised by PGP activity, by reducing or increasing PGP activity in a cell. PGP nucleic are used as oligonucleotide probes. Complements of PGP nucleic acids are useful as antisense oligonucleides, to induce a PGP acids are useful as antisense oligonucleides.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Patten CJ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Dog; P-glycoprotein allelic variant; PGP; multidrug transporter;
MDR1; drug bioavailability; transgenic animal; genetic model.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 12.5%; Score 69; DB 22; Length 1281;
25.5%; Pred. No. 70;
tive 12; Mismatches 33; Indels 28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /note= "His of GenotypeC substituted by Gln"
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                                                                                                                                                                                                                                                                                                                                                                                                               Dog P-glycoprotein (PGP) allelic variant (Genotype A).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Reif TC,
                                                           396 FKNVHFSYPSRKEVKILKGLNLKVQSGQTVALVGNSGC 433
75
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   -----TGQTAALYNQAGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Claim 17; Page 91-93; 111pp; English.
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                                                                                                                                                                                                                             AAE00308 standard; Protein; 1281
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            99US-0156510
                                                                                                                                                                                                                                                                                                                                                       (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WPI; 2001-235373/24.
   60 ----FSY-----
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Matches 25; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1281 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Misc-difference 197
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Canis familiaris.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WO200123540-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               28-SEP-1999;
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                                                                                                                                                                                                                                                                                                                                                    13-JUN-2001
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                                                                                                                                                                                                                                                                                               AAE00308;
                                                                                                                                                                 RESULT 13
                                                                                                                                                                                                  AAE00308
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New dog P-glycoproteins (PGP) and their encoding nucleic acids, useful for determining the bioavailability of drugs and for screening for dog
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The invention relates to dog P-glycoprotein (PGP) also referred as multidrug transporter (MDR1) and nucleic acids encoding them. The invention also includes fragments and biologically functional variants of dog P-glycoprotein. PGP and their nucleic acids are useful for determining the bioavailability of drugs and for screening PGP inhibitors. They are useful for the diagnosis and treatment of conditions characterised by PGP activity, by reducing or increasing PGP activity in a cell. PGP nucleic acids are used as oligonucleotide probes. Complements of PGP nucleic acids are useful as antisense oligonucleotides, to induce a PGP 'knockout' phenotype. They are used to prepare a non-human transgenic animal, which are valuable as genetic models for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The present sequence is dog P-glycoprotein (PGP) allelic variant. This sequence is also referred as Genotype B protein. The PGP enzyme functions as an efflux pump exporting small molecules across the cell membrane. This enzyme is a member of the ABC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Patten CJ;
                                                                                                                                                                                                                                                                 Dog, P-glycoprotein allelic variant, PGP, multidrug transporter, MDR1, drug bioavailability, transgenic animal, genetic model.
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                                                                                                                                                                                                                                                                                                                                                                                          'note= "Asn of GenotypeC substituted by Lys"
                                                                                                                                                                                                                                                                                                                                                                                                                           /note= "His of GenotypeC substituted by Gln"
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                                                                                                                                                                                                                             Dog P-glycoprotein (PGP) allelic variant (Genotype B)
                             396 FKNVHFSYPSRKEVKILKGLNLKVQSGQTVALVGNSGC 433
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----FSY----TGQTAALYNQAGC
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Misc-difference 25
                                                                                                                         AAE00309 standard; Protein; 1281 AA
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                                                                                                                                                                                                                                                                                                                     Canis familiaris.
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                                                                                                                                                            AAE00309;
9
                                                                                       RESULT 14
                                                                                                          AAE00309
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Gaps

28;

6 LFFSVITVMMLIAMASEMV-----NGSAFTVWSGPGCNNRAERYSKCGCSAIHQKGGYD 59

25; Conservative

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RESULT 15
AAE00310
AAE00310
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                                                                                                                               The invention relates to dog P-glycoprotein (PGP) also referred as multidrug transporter (MDR1) and nucleic acids encoding them. The invention also includes fragments and biologically functional variants of dog P-glycoprotein. PGP and their nucleic acids are useful for determining the bioavailability of drugs and for creatment of conditions characterised by PGP activity, by reducing or increasing PGP activity in a cell. PGP nucleic acids are used as oligonucleotide probes. Complements of PGP nucleic acids are useful as antisense oligonucleotides, to induce a PGP 'knockout' phenotype. They are used to prepare a non-human transgenic animal, which are valuable as genetic models for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        New dog P-glycoproteins (PGP) and their encoding for determining the bioavailability of drugs and PGP inhibitors - {\sf PGP}
                       human diseases.
The present sequence is dog P-glycoprotein (PGP) allelic variant.
This sequence is also referred as Genotype D protein. The PGP
enzyme functions as an efflux pump exporting small molecules
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Claim 17; Page 108-110; 111pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Dog P-glycoprotein (PGP) allelic variant
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            396 FKNVHFSYPSRKEVKILKGLNLKVQSGQTVALVGNSGC 433
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         note= "His of GenotypeC
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                                                                                                                                   Query Match
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  396
                                                      336 VFFSVLIGAFSIGQASPSIEAFANARGAAYEIFKIIDNKPSIDSYSKSGHKPDNIKGNLE 395
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                                                                                6 LFFSVITVMMLIAMASEMV-----NGSAFTVWSGPGCNNRAERYSKCGCSAIHQKGGYD 59
FKNVHFSYPSRKEVKILKGLNLKVQSGQTVALVGNSGC
                              ----FSY-----
                                                                                                                                                               1281 AA;
                                                                                                          Conservative
                                                                                                                       12.5%;
                             ----TGQTAALYNQAGC
                                                                                                          12; Mismatches
                                                                                                                       Score 69; DB
Pred. No. 70;
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    433
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Search completed: January 12, 2003, 09:35:53 Job time : 68 secs

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Perfect score:
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Maximum Match 100%
Listing first 45 summaries
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Maximum DB seq length: 2000000000
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ore greater than or equal to the score of the result being printed,
is derived by analysis of the total score distribution.
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    Issued Patents AA:*

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| CGD2_6/ptcdata/1/iaa/6A_COMB.pep:*
| CGD2_6/ptcdata/1/iaa/6A_COMB.pep:*
| CGD2_6/ptcdata/1/iaa/POTUS_COMB.pep:*
| CGD2_6/ptcdata/1/iaa/backfIles1.pep:*
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Copyright (c) 1993 - 2003 Compugen Ltd
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US-07-872-678A-48
US-08-583-276-19
US-08-752-447-2
US-08-752-447-2
US-09-316-167-2
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US-08-596-014A-4
US-08-596-014A-2
US-08-8877-620-2
US-08-8877-620-2
US-08-8877-620-2
US-08-8877-6280-2
US-08-8877-6280-2
US-08-8877-6280-2
US-09-347-833-11
US-08-680-2270-4
US-08-857-2248-98
US-07-857-2248-98
US-07-857-2248-98
US-08-144-121-4
US-08-7857-6248-98
US-08-7857-6248-98
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US-08-7857-6248-98
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US-08-735-893-4
US-08-680-326-41
US-08-680-326-41
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Sequence 2, Appli
Sequence 2, Appli
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Patent No. 5206352
Sequence 4, Appli
Sequence 4, Appli
Sequence 4, Appli
Sequence 2, Appli
Sequence 2, Appli
Sequence 9, Appli
Sequence 105, Appli
Sequence 105, Appli
Sequence 98, Appli
Sequence 4, Appli
Sequence 4, Appli
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Sequence
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	uery Match 13.5%; Score 74.5; DB 1; Length 486 est Local Similarity 39.3%; Pred. No. 1.1; atches 24; Conservative 4; Mismatches 18; Indels	REGISTRATION NUMBER: 36,111 REFERENCE/DOCKET NUMBER: ARCDO16 TELECHOMUNICATION INFORMATION: TELEPHONE: 713-787-1400 TELEPEAX: 79-0924 TELEX: 79-0924 TELEX: 79-0924 INFORMATION FOR SEQ ID NO: 48: SEQUENCE CHARACTERISTICS: LENGTH: 486 amino acids TYPE: amino acids TYPE: amino acids TYPE: amino acid STRANDEDNESS: single TOPOLOGY: linear MOLECULE TYPE: DNA (genomic) 07-872-678A-48	COUNTRY: USA COUNTRY: USA ZIP: 77210 COMPUTER READABLE FORM: MEDIUM TYPE: Floppy disk COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: PStentin Release #1.0, Version #1.25 CURRENT APPLICATION DATA: APPLICATION NUMBER: US/07/872,678A FILING DATE: 2-APRI-1992 CLASSIFICATION: 435 ATTORNEY/AGENT INFORMATION: NAME: CONSTITUTE TO THE PROPERTY OF THE PROPERTY O	SULT 1 107-872-678A-48 Sequence 48, Application US/07872678A Sequence 48, Application US/07872678A Sequence 48, Application US/07872678A SERVERAL INFORMATION: APPLICANT: Bell, Graeme, et al. TITLE OF INVENTION: DETECTION OF EARLY-ONSET TITLE OF INVENTION: NON-INSULIN-DEPENDENT DIABETES MELLITUS NUMBER OF SEQUENCES: 48 CORRESPONDENCE ADDRESS: ADDRESSEE: Arnold, White & Durkee STREET: Post Office Box 4433 CITY: Houston	28 60 10.9 871 4 US-09-245-041-19 Sequence 60 10.9 1198 4 US-09-245-041-131 Sequence 61 10.9 1198 4 US-09-245-041-131 Sequence 62 10.9 1198 4 US-09-245-041-17 Sequence 62 10.9 1198 4 US-09-245-041-17 Sequence 62 10.9 2787 4 US-09-245-041-15 Sequence 62 10.9 2787 4 US-09-245-041-15 Sequence 62 10.9 2787 4 US-09-245-041-15 Sequence 62 10.7 352 2 US-08-960-960-961-12 Sequence 62 10.7 352 2 US-08-960-961-12 Sequence 63 10.7 1260 4 US-09-245-041-12 Sequence 64 10.5 10.6 110.6 110.6 US-09-134-001C-3957 Sequence 64 10.5 10.6 1
FG 94 : LKDIYG 440	; 15; Gaps 4			ω	ence 19, Applence 131, Applence 17, Applence 17, Applence 12, Applence 11, Applence 11, Applence 11, Applence 12, Applence 14, Applence 14, Applence 2, Applence 2, Applence 3, Applence 357, Appence 4541, Appence 377, Appence 377, Appence 377, Appence 377, Appence 2, Applence 377, Appence 2, Applence 2, Applence 377, Appence 2, Applence 2, A

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COUNTRY:
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Patent No. 5994088

GENERAL INFORMATION:
APPLICANT: Mechetner, Eugene
APPLICANT: Roninson, Igor B
TITLE OF INVENTION: Wethods and Reagents for Preparing and
TITLE OF INVENTION: Using Immunoligcal Agents Specific for P-glycoprotein
NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                334 VFFSVLIGAFSVGQAŠPSIEAFANARGAAYEIFKIIDNKPSIDSYSKSGHKPDNIKGNLE 393
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                                                                                                                                                                                                                                                                                       APPLICANT: Michauis, Arthur
APPLICANT: Nichhuis, Arthur
APPLICANT: Nichhuis, Arthur
APPLICANT: Tolstoshev, Paul
TITLE OF INVENTION: IMPROVED EXPRESSION OF HUMAN
TITLE OF INVENTION: MULTIDRUG RESISTANCE GENES AND IMPROVED
TITLE OF INVENTION: SELECTION OF CELLS TRANSDUCED WITH SUCH GENES
OVERESPONDENCE: 19
CORRESPONDENCE ADDRESS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ADDRESSEE: Carella, Byrne, Bain, Gilfillan, ADDRESSEE: Cecchi & Stewart STREET: 6 Becker Farm Road
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER: IBM PS/2
OPERATING SYSTEM:
OPERATING SYSTEM:
OPERATING SYSTEM:
SOFTWARE:
DM4 V2
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/583,276
FILING DATE: 05-JAN-1996
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/332,444
FILING DATE: 21-0CT-1994
APPLICATION NUMBER: 07/887,712
FILING DATE: 22-MAY-1992
INFORMATION FOR SEQ ID NO: 19:
SEQUENCE CHARACTERISTICS:
LENGTH: 1280 amino acids
TYPE: amino acid
                                                                                                                                                                                                   Sequence 19, Application US/08583276
Patent No. 5837536
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch diskette
COMPUTER: IBM PS/2
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: New Jersey
RY: USA
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US-08-583-276-19
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US-08-752-447-2
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                                                       441 W 441
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STATE:
95 W 95
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APPLICANT: Mecherner, Eugene
APPLICANT: Roninson, Igor B
TITLE OF INVENTION: Methods and Reagents for Preparing and
TITLE OF INVENTION: Using Immunoligcal Agents Specific for P-glycoprotein
NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
STREET: 300 South Wacker Drive, Seventh Floor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  6 LFFSVITVMMLIAMASEMV-----NGSAFTVWSGPGCNNRAERYSKCGCSAIHQKGGYD 59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       12.3%; Score 68; DB 2; Length 1280; 24.5%; Pred. No. 21;
ADDRESSEE: McDonnell Boehnen Hulbert & Berghoff Ltd.
STREET: 300 South Wacker Drive, Seventh Floor
                                                                                                       ZIP: 60606
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION NUMBER: US/08/752,447
FILING DATE: 15-NOV-1996
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COMPUTER: Floppy disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
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                                                                                                                                                                                                                                                                                      APPLICALLY
FILING DATE: 15-NOV-1996
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: No. 5994008man, Kevin E
REGISTRATION NUMBER: 35,303
REFERENCE/DOCKET NUMBER: 95,1121
TELEPHONE: 312-913-9008
TELEFAX: 312-913-9008
INFORMATION FOR SEQ ID NO: 2: SEQUENCE CHARACTERISTICS:
SEQUENCE CHARACTERISTICS:
LENGTH: 1280 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/316,167
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CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/752,447
FILING DATE: 15-NOV-1996
ATTORNEY/AGENT INFORMATION:
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Patent No. 6365357
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       24; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TOPOLOGY: linear
MOLECULE TYPE: protein
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
    ADDALL
STREET: 300
CITY: Chicago
STATE: Illinois
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Matches 24; Conserva
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STATE: Illinois
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                                                                                                                                                                                                                                                      RESULT 6
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TITLE OF INVENTION: COMPOSITIONS FOR CLONES CONTAINING DNA
SEQUENCES ASSOCIATED WITH MULTIDRUG RESISTANCE IN HUMAN CELLS
NUMBER OF SEQUENCES: 4
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  US-09-316-167-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQ ID NO:4:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Michael M.
                                                                                                                                              Sequence 2, Application US/08701846
PATENT NO. 5717069
GENERAL INFORMATION:
APPLICANT: Granados, Robert R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Patent No. 5206352
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Matches
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          NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
ADDRESSEE: Barnard, Brown & Michaels
STREET: 306 E. State St., Suite 220
                                                                             APPLICANT: Granados, Robert R.
TITLE OF INVENTION: WHICH ENHANCES VIRUS INFECTION OF HOST INSECTS
NUMBER OF SEQUENCES: 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICATION NUMBER: US/07/622,836 FILING DATE: 24-SEP-1990 PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Roninson, Igor B.; Pastan Ira H.; Gottesman,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE CHARACTERISTICS:
LENGTH: 1280 amino aci
                                                                                                                                                                                                                                                                                                                                                                                     334 VFFSVLIGAFSVGQASPSIEAFANARGAAYEIFKIIDNKPSIDSYSKSGHKPDNIKGNLE 393
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                       394 FRNVHFSYPSRKEVKILKGLNLKVQSGQTVALVGNSGC 431
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       334 VFFSVLIGAFSVGQASPSIEAFANARGAAYEIFKIIDNKPSIDSYSKSGHKPDNIKGNLE 393
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       394 FRNVHFSYPSRKEVKILKGLNLKVQSGQTVALVGNSGC 431
                                                                                                                                                                                                                                                                                                                                              60 -----F$Y-------TGQTAALYNQAGC 75
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICATION NUMBER: 892,575
FILING DATE: 01-AUG-1986
APPLICATION NUMBER: 845,610
FILING DATE: 28-MAR-1986
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   60 ----FSY-----TGQTAALYNQAGC 75
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NAME: No. 6365357nan, Kevin E
REGISTRATION NUMBER: 35,303
REFERENCE/DOCKET NUMBER: 95,1121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LENGTH: 1280
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              6 LFFSVITVMMLIAMASEMV-----NGSAFTVWSGPGCNNRAERYSKCGCSAIHQKGGYD 59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Match 12.3%; Score 68; DB 4; Length 1280; Local Similarity 24.5%; Pred. No. 21;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TELEFAX:
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Ithaca,
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RESULT 7
US-08-296-014A-4
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
rocal Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                        GENERAL INFORMATION:
APPLICANT: Ding,
APPLICANT: Ho, Bo
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICATION NUMBER: 60/002,743
FILING DATE: 24-AUG-1995
ATTORNEY_AGENT INFORMATION:
NAME: Michaels, Christopher A.
REGISTRATION NUMBER: 34,390
REFERENCE/DOCKET NUMBER: BTI-32
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: HO, BOW
TITLE OF INVENTION:
TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER: US
FILING DATE: 23-AUG-19
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
ATTORNEY/AGENT INFORMATION:
NAME: Murphy, Jr., Gerald M.
REGISTRATION NUMBER: 28,977
                                                                                                         OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                 ZIP: 22042
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: amino acids
TOPOLOGY: limited
MOLECHT 912
                                                                                                                                                                                                                                                                                                                             NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
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LENGTH: 902 amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA: APPLICATION NUMBER: US/08/701,846
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy of COMPUTER: IBM PC comp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        273 QYTWMNKTKR 282
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           213 GGAYYGAFWTAPASTNLGEYLRVSPTNWMVIHELGHAYDFVFTVNTRLIEIWNNSFCDRI 272
                                                                                                                                                                                                                                                            STREET: 8110 Gateho
CITY: Falls Church
STATE: Virginia
                                                     CLASSIFICATION:
                                                                           FILING DATE:
                                                                                      APPLICATION NUMBER: US/08/296,014A
                                                                                                                                                                   COMPUTER:
                                                                                                                                                                                                                                       COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              79 AHTREGSSAR 88
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            26 GSAF--TVWSGPGCNNRAE--RYSKCGCSAIHQKG-GYDFSYTGQT--AALYNQAGCSGV 78
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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Y: USA
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                                                                                                                                                                                                                                                                                         8110 Gatehouse Road,
                                                                                                                                                                                                                                                                                                                                                                                                                        Ding, Jeak Ling
Ho, Bow
                                                                                                                                          E: Floppy disk
IBM PC compatible
SYSTEM: PC-DOS/MS-DOS
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                                                       435
                                                                                                                                                                                                                                                                                                                                                        The Cloned Factor C cDNA of the Singapore Horseshoe Crab, Carcinoscorpius rotundicauda and Purification of Factor C Proenzyme
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   12.3%; Score 67.5; D
28.6%; Pred. No. 16;
tive 10; Mismatches
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                                                                                                                                                                                                                                                                                           Suite 500 East
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DB 1; Length 902;
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us-09-882-434a-1.rai

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Sequence 4, Application US/08596405
Sequence 7, Application US/08596405
Setent No. 5858706
GENERAL INFORMATION:
APPLICANT: Ding, Jeak Ling
APPLICANT: Ho, Bow
TITLE OF INVENTION: The Cloned Factor C cDNA of the
TITLE OF INVENTION: Singapore Horseshoe Crab, Carcinoscorpius
TITLE OF INVENTION: Totundicauda and Purification of Factor C Proenzyme
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             32 WSG--PGCNNRAERYSKCGCSAIHQKGGYDF-SYTGQTAALYNQAGCSGVAHTRFGSS 86
                                                                                                                                                                                                                                                                                                                                                     32 WSG--PGCNNRAERYSKCGCSAIHQKGGYDF-SYTGQTAALYNQAGCSGVAHTRFGSS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity 32.8%; Pred. No. 54;
Matches 19; Conservative 8; Mismatches 22; Indels 9;
                                                                                                                                                                                                                                                                   11.5%; Score 63.5; DB 1; Length 1019; 32.8%; Pred. No. 54; tive 8; Mismatches 22; Indels 9;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/596,405
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STREET: Birch, Stewart, Kolasch & Birch STREET: 8110 Gatehouse Road, Suite 500 East CITY: Falls Church STATE: Virginia
    1781-105P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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FILING DATE:
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Murphy, Jr., Gerald M.
REGISTRATION NUMBER: 28,977
REFERENCE/DOCKET NUMBER: 1781-
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 205-8000
"FIREFAX: (703) 205-8050
REFERENCE/DOCKET NUMBER: 171
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 205-8050
TELEFAX: (703) 205-8050
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELEX: 248345
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 1019 amino acids
                                                              TELEFAX: (703) 205-8050
TELEX: 248345
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                  1019 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: amino acid

TOPOLOGY: linear

, MOLECULE TYPE: protein

US-08-596-405-4
                                                                                                                                                                                                                                                                                                                    19; Conservative
                                                                                                                                                                                         TOPOLOGY: linear MOLECULE TYPE: protein
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                                                                                                                                                                      amino acid
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                                                                                                                                                     LENGTH:
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APPLICANT: Ding, Jeak Ling
APPLICANT: Ho. Bow
TITLE OF INVENTION: The Cloned Factor C cDNA of the
TITLE OF INVENTION: Singapore Horseance Crab, Carcinoscorpius
TITLE OF INVENTION: rotundicauda and Purification of Factor C Proenzyme
NUMBER OF SEQUENCES:
ADDRESSEB: Birch, Stewart, Kolasch & Birch
STREET: Bilo Catehouse Road, Suite 500 East
CITY: Falls Church
STATE: Virginia
                                                                 GENERAL INFORMATION:
APPLICANT: Ding, Jeak Ling
APPLICANT: Ding, Jeak Ling
APPLICANT: Ding, Jeak Ling
APPLICANT: Bow
TITLE OF INVENTION: The Cloned Factor C cDNA of the
TITLE OF INVENTION: Singapore Horseshoe Crab, Carcinoscorpius
TITLE OF INVENTION: rotundicauda and Purification of Factor C Proenzyme
NUMBER OF SEQUENCES:
ADDRESSEE: Birch, Stewart, Kolasch & Birch
STREET: 8110 Gatehouse Road, Suite 500 East
CITY: Falls Church
STATE: Virginia
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query March
Best Local Similarity 32.8%; Pred. No. 54;
Matches 19; Conservative 8; Mismatches 22; Indels 9;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SOFTWARE: Patentin Release #1.0, Version #1.25 CURRENT APPLICATION DATA: APPLICATION NUMBER: US/08/877,620 FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1781-105P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ; Sequence 2, Application US/08296014A; Patent No. 5716834; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NAME: Murphy, Jr., Gerald M.
REGISTRATION NUMBER: 28,977
REPERSONE/DOCKET NUMBER: 1781-
TELECHMUNICATION:
TELEPHANE: (703) 205-8050
TELEFAX: (703) 205-8050
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/596,405
                ; Sequence 4, Application US/08877620 ; Patent No. 5985590
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELEX: 248345
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 1019 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                            ZIP: 22042
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FILING DATE: ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MOLECULE TYPE: protein
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                                                                                                                                                                                                                                                                                                                                                                                         COUNTRY:
US-08-877-620-4
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GENERAL INFORMATION:
APPLICANT: Ding, Jeal
APPLICANT: Ho, Bow
TITLE OF INVENTION:
TITLE OF INVENTION:
TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 2, Application US/08596405
Patent No. 5858706
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
                                                                                            CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: MUIPPY, Jr., Gerald M.
REGISTRATION NUMBER: 28,977
REFERENCE/OCKET NUMBER: 1781-
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 205-8000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELEFAX: (703) 205-80
TELEX: 248345
INFORMATION FOR SEQ ID NO:
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 1083 amino acids
                                                                                                                                                                                                                                                                                                                                                                                             STREET: 8110 C.
STREET: Palls Church
STATE: Virginia
COUNTRY: USA
                                                                                                                                                                                                                                                                  COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: ISM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
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LENGTH: 1083 amino aci
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TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 205-8000
TELEFAX: (703) 205-8050
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MOLECULE TYPE: protein
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MEDIUM TYPE: Floppy disk
                                        TELLEFAX: 248345
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                378 WSGSQPSCVKVADREVDCDSKAV-----DFLDDVGEPVRIHCPAGCSLTAGTVWGTA 429
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NAME: Murphy, Jr., Gerald M. REGISTRATION NUMBER: 28,977
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FILING DATE:
CLASSIFICATION: 435
                                                                                                                                                                                                                                                    APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICATION NUMBER:
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XGY: linear
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8110 Gatehouse Road, Suite 500 East
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                                                                          (703) 205-8050
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32.8%;
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Singapore Horseshoe Crab, Carcinoscorpius
rotundicauda and Purification of Factor C Proenzyme
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Pred. No. 58;
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RESULT 13
US-07-857-224B-99
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US-08-877-620-2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 2, Application US/08877620 Patent No. 5985590
                                                                                                                                                                   Query Match
                                                                                                                                     Matches
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APPLICANT: Ding, applicant: Ho, Bo
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Matches 19; Conserv
                                                                                                                                                                                                                                                                                                      INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ZIP: 22042
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compactible
OPERATING SYSTEM: PC-DOS/MS-DOS
OPERATING SYSTEM: PC-BOS #1.0,
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TOPOLOGY: linear
MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CLASSIFICATION: PRIOR APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TITLE OF INVENTION:
TITLE OF INVENTION:
                                                                                                                                                                                                                 MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                   SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                    REFERENCE/DOCKET NUMBER: 1781-105P
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 205-8000
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CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/877,620
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                                                                                                                                                                                                                                                                                                        TELEFAX: 248345
                                                                 378 WSGSOPSCVKVADREVDCDSKAV-----DFLDDVGEPVRIHCPAGCSLTAGTVWGTA 429
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                                                                                                                           11.5%;
Local Similarity 32.8%;
les 19; Conservation
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                                                                                                 32 WSG--PGCNNRAERYSKCGCSAIHQKGGYDF-SYTGQTAALYNQAGCSGVAHTRFGSS 86
                                                                                                                                                                                                                                      TOPOLOGY:
                                                                                                                                                                                                                                                  TYPE: amino acid
                                                                                                                                                                                                                                                                    LENGTH:
                                                                                                                                                                                                                                                                                                                        TELEPHONE: (703) 205-8050
                                                                                                                                                                                                                                                                                                                                                                                                    NAME: Murphy, Jr., Gerald M. REGISTRATION NUMBER: 28,977
                                                                                                                                                                                                                                                                                                                                                                                                                                                          FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CITY: Falls Church
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ADDRESSEE: Birch, Stewart, Kolasch & Birch
STREET: 8110 Gatehouse Road, Suite 500 East
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Ho, Bow
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The Cloned Factor C cDNA of the Singapore Horseshoe Crab, Carcinoscorpius rotundicauda and Purification of Factor C
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Pred. No. 58;
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Pred. No. 58;
                                                                                                                                   Mismatches
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                                                                                                                                                                   DB 2;
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                                                                                                                                   22;
                                                                                                                                                                 Length 1083;
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                                                                                                                                   Indels
                                                                                                                                  9
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; Sequence 99, Application US/07857224B
; Patent No. 5958784

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STATE: IN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RESULT 15
US-08-804-227C-4
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                                                                                                                             LENGTH: 442
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5: Dixon, D. C.
5: Carr, J. P.
7: Klessig, D. F.
1: Klessig, D. F.
1: Solation and nucleotide sequence of CDNA clones for the pathogenesis related proteins of Nicotiniana tabacum induced by TMV
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31.2%; Pred. No. 5.8;
tive 5; Mismatches 24; Indels 37; Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             39 NRAERY--SKCG-CSAIHQ-----KGGYDFSYTGQTAAL-----YNQA--GCSG- 77
                                                                                                                                                                                                              COMPUTER READABLE FORM:

MEDIUM TYPE: 3.5 indicate, 1.4 Mb storage
COMPUTER: Apple MacIntosh
COMPUTER: Apple MacIntosh
COMPUTER: Apple MacIntosh
COMPARE: Microsoft Word
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/857,224B
FILING DATE: 03/25/92
CLASSIFICATION DATA: none
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECHNONE: (International) 41 1 632 2830
TELEFRONE: (International) 41 1 262 2437
             APPLICANT: Benner, Steven A.

TITLE OF INVENTION: Predicting Folded Structures of Proteins
NUMBER OF SEQUENCES: 114
CORRESPONDENCE ADDRESS:
ADDRESSEE: Steven A. Benner
STREET: Hadlaubstrasse 151
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ORGANISM: Lycopersicon esculentum
FEATURE: Pathogenesis related protein; Table 16 Row 3
PUBLICATION INFORMATION:
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Sequence 11, Application US/09347833

Sequence 11, Application US/09347833

Fatent No. 6294684

GENERAL INFORMATION:

APPLICANT: Famodu, Layo O.

APPLICANT: Odell, Joan T.

TITLE OF INVENTION: Factors Involved in Gene Expression; FILE REFERENCE: BB-1172

CURRENT APPLICATION NUMBER: US/09/347,833
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Matches 30; Conservative
                                                                                                                                                                         STATE: none
COUNTRY: Switzerland
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               protein
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GENERAL INFORMATION:
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                                                                                                                                                      Zurich
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DESCRIPTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PAGES: 9861
DATE: 1988
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JOURNAL:
VOLUME: 1
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AUTHORS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                     326 MMMVGRAGRRAGAGGMSMMGMGRGGGRGYRYTCRGMDAMHGVGGVMTSYMG---GMMRDA 382
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                                                                                                                                                                                                                                                                                                                                                                                                      14 MMLIAMASEMVNGSAFTVWSGPGCNNRAERYSKCGCSAIHQKGGYDFSYTGQTAALYNQA 73
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28.8%; Pred. No. 4e+02;
                                                                                                                                                                                                                                                                                                Query Match 11.3%; Score 62; DB 4; Length 442; Best Local Similarity 25.9%; Pred. No. 28; Matches 21; Conservative 9; Mismatches 43; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Bosteck, Bradley S.
APPLICANT: Kuhstoss, Stuart A.
APPLICANT: Rosteck, Paul R., Jr.
APPLICANT: Sutton, Kimberly L.
TITLE OF INVENTION: POLYKETIDE SYNTHASE GENES
NUMBER OF SEQUENCES: 15
CORRESPONDENCE ADDRESS:
ADDRESSEE: THOMAS G. PLANT 1501
STREET: LILLY CORPORATE CENTER
CITY: INDIANAPOLIS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        10; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMMUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM Compartible
OPERATING SYSTEM: MS-DOS
SOFTWARE: ASCI (DOS) Text only
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/804,227C
FILING DATE: February 21, 1997
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Plant, Thomas, G.
REGISTRATION NUMBER: 35,784
REFERENCE/DOCKET NUMBER: X-8231
CURRENT FILING DATE: 1999-07-02
EARLIER APPLICATION NUMBER: 60/092,415
EARLIER FILING DATE: July 10, 1998
NUMBER OF SEQ ID NOS: 11
SOFFWARE: Microsoft Office 97
SEQ ID NO 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 4, Application US/08804227C; Patent No. 5876991; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TELECOMMUNICATION INFORMATION.
TELEPHONE: 317-276-2459
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 383 GSVGAA----SAANSTRMMG 398
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               74 GCSGVAHTRFGSSARACNPFG 94
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                                                                                                                                                                                         ; TYPE: PRT
; ORGANISM: Triticum aestivum
US-09-347-833-11
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Best Local Similarity 28.84
Matches 21; Conservative
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Search completed: January 12, 2003, 09:40:11 Job time : 28 secs

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Database
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Perfect score:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Minimum DB seq length: 0
Maximum DB seq length: 200000000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      OM protein - protein search, using sw model
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Scoring table:
Published Applications AA:*

1: /cgn2 6/ptodata/2/pubpaa/USO8 NEW PUB.pep:*

2: /cgn2 6/ptodata/2/pubpaa/USO8 NEW PUB.pep:*

3: /cgn2 6/ptodata/2/pubpaa/USO6 NEW PUB.pep:*

4: /cgn2 6/ptodata/2/pubpaa/USO6 PUBCOMB.pep:*

5: /cgn2 6/ptodata/2/pubpaa/USO7 NEW PUB.pep:*

6: /cgn2 6/ptodata/2/pubpaa/USO7 PUBCOMB.pep:*

6: /cgn2 6/ptodata/2/pubpaa/USO7 PUBCOMB.pep:*

7: /cgn2 6/ptodata/2/pubpaa/USO7 PUBCOMB.pep:*

9: /cgn2 6/ptodata/2/pubpaa/USO9 PUBCOMB.pep:*

9: /cgn2 6/ptodata/2/pubpaa/USO9 PUBCOMB.pep:*

10: /cgn2 6/ptodata/2/pubpaa/USO9 PUBCOMB.pep:*

11: /cgn2 6/ptodata/2/pubpaa/USO9 PUBCOMB.pep:*

12: /cgn2 6/ptodata/2/pubpaa/USO9 PUBCOMB.pep:*

13: /cgn2 6/ptodata/2/pubpaa/USO9 PUBCOMB.pep:*

14: /cgn2 6/ptodata/2/pubpaa/USO9 PUBCOMB.pep:*
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551
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Maximum Match 100%
Listing first 45 summaries
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GenCore version 5.1.3
Copyright (c) 1993 - 2003 Compugen Ltd
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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61	64	64	64	64.5	68	68	68	69	70.5	75.5	415	417	419	421	426	426	426	551	Score
11.1	11.6	11.6	11.6	11.7	12.3	12.3	12.3	12.5	12.8	13.7	75.3	75.7	76.0	76.4	77.3	77.3	77.3	100.0	Query Match Length
501	1609	1272	1272	147	1280	1280	1280	1280	267	486	76	76	76	76	76	76	76	102	
œ	10	10	10	φ	10	10	9	9	9	10	10	10	10	10	10	10	10	10	BB
US-08-635-967-2	US-09-938-275-11	US-09-769-097-4	US-09-769-097-2	US-10-016-634A-115	US-09-866-866A-4	US-09-866-866A-2	US-10-072-621-7	US-10-044-671-2	US-09-764-868-1164	US-09-801-368-154	US-09-882-434A-20	US-09-882-434A-21	US-09-882-434A-18	US-09-882-434A-19	US-09-882-434A-17	US-09-882-434A-16	US-09-882-434A-15	US-09-882-434A-1	ID
Sequence 2, Appli	μ.	•	Sequence 2, Appli	115	4.	Sequence 2, Appli	Sequence 7, Appli	Sequence 2, Appli	Sequence 1164, Ap	154	Sequence 20, Appl	Sequence 21, Appl	Sequence 18, Appl	Sequence 19, Appl	Sequence 17, Appl	Sequence 16, Appl	Sequence 15, Appl	Sequence 1, Appli	Description

ALIGNMENTS

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APPLICANT: MANNERS, John M.
APPLICANT: MARCUS, John Paul
APPLICANT: MARCUS, John Paul
APPLICANT: Goulter, Kenneth C.
APPLICANT: Green, Jodie Lyn
TITLE OF INVENTION: ANTI-MICROBIAL PROTEIN
FILE REFERENCE: CULLNI8.1CP1C1
CURRENT APPLICATION UNMBER: US/09/882,434A
CURRENT FILING DATE: 2001-06-15
PRIOR APPLICATION NUMBER: 09/364395
PRIOR FILING DATE: 1999-07-30
PRIOR APPLICATION NUMBER: 09/117615
PRIOR FILING DATE: 1998-11-09
PRIOR APPLICATION NUMBER: PCT/AU97/00052
PRIOR FILING DATE: 1997-01-31
PRIOR APPLICATION NUMBER: AU PN 7802
PRIOR APPLICATION NUMBER: AU PN 7802
PRIOR FILING DATE: 1996-01-31
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                                                                                                                                                                                          Query Match 100.0%; Score 551; DB 10; Best Local Similarity 100.0%; Pred. No. 4.1e-57; Matches 102; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                  NUMBER OF SEQ ID NOS: 21
SOFTWARE: FRATSEQ for Windows Version 4.0
SEQ ID NO 1
LENGTH: 102
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                    TYPE: PRT
ORGANISM: Macadamia integrifolia
       61
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                                                                                                                     1 MASTKLFFSVITVMMLIAMASEMVNGSAFTVMSGPGCNNRAERVSKCGCSAIHQKGGYDF 60
                                                                                           SYTGQTAALYNQAGCSGVAHTRFGSSARACNPFGWKSIFIQC 102
                              SYTGQTAALYNQAGCSGVAHTRFGSSARACNPFGWKSIFIQC 102
                                                                                                                                                                                                                                          Length 102;
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75; Conservative
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              OTHER INFORMATION: Mi28K variant. Variant MiAMP1 protein Mi28K OTHER INFORMATION: containing a Lysine at amino acid 28 (used primer OTHER INFORMATION: from SEQ ID NO:8 to produce).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 76;
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Sequence 16, Application US/09882434A

Patent No. US20020108144A1

GENERAL INFORMATION:
APPLICANT: Manners, John M.
APPLICANT: Goulter, Kenneth C.
APPLICANT: Green, Jodin Paul
APPLICANT: Green, John E.
CURRENT FILING DATE: 2001-06-15
PRIOR APPLICATION NUMBER: 09/364395
PRIOR FILING DATE: 1999-07-30
PRIOR FILING DATE: 1998-11-09
SPRIOR FILING DATE: 1998-11-09
APRIOR APPLICATION NUMBER: AU PN 7802
PRIOR APPLICATION NUMBER: AU PN 7802
PRIOR APPLICATION NUMBER: AU PN 7802
PRIOR FILING DATE: 1996-01-31
NUMBER OF SEQ ID NOS: 21
SCOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 16
            US-09-882-434A-15

US-09-882-434A-15

Sequence 15. Application US/09882434A

Patent No. US2002010814A1

GENERAL INFORMATION:

APPLICANT: Mancus, John Paul

APPLICANT: Marcus, John Paul

APPLICANT: Green, Jodie Lyn

TITLE OF INVENTION: ANTI-MICROBIAL PROTEIN

FILE REFERENCE: CULLANIB ..PCIC.

CURRENT FILING DATE: 2001-06-15

PRIOR APPLICATION NUMBER: 09/364395

PRIOR APPLICATION NUMBER: 09/117615

PRIOR APPLICATION NUMBER: 09/117615

PRIOR FILING DATE: 1999-07-30

PRIOR FILING DATE: 1999-101-09

PRIOR FILING DATE: 1999-101-31

PRIOR FILING DATE: 1997-01-31

PRIOR FILING DATE: 1996-01-31

NUMBER OF SEQ ID NOS: 21

NUMBER OF SEQ ID NOS: 21
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ORGANISM: Artificial Sequence
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ORGANISM: Artificial Sequence
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LENGTH: 76
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OTHER INFORMATION: Mi39K variant. Variant MiAMPl protein Mi39K oTHER INFORMATION: containing a Lysine at amino acid 39 (used primer ) OTHER INFORMATION: from SEQ ID NO:9 to produce).
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                                                                                                                                          77.3%; Score 426; DB 10; Length 76; 98.7%; Pred. No. 9.3e-43; tive 1; Mismatches 0; Indels
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98.7%; Pred. No. 9.3e-43;
tive 1; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FILE REFERENCE: CULTURENT SOUR STATE CURRENT APPLICATION NUMBER: US/09/882,434A CURRENT FILING DATE: 2001-06-15 PRIOR APPLICATION NUMBER: 09/364395 PRIOR FILING DATE: 1999-07-30 PRIOR FILING DATE: 1999-07-30 PRIOR FILING DATE: 1998-11-09 PRIOR FILING DATE: 1997-01-31 PRIOR FILING DATE: 1996-11-03 PRIOR FILING DATE: 1996-11-03 PRIOR FILING DATE: 1996-01-31 NUMBER OF SEQ ID NOS: 21 SOFTWARE: FABLESC FOR WINDOWS VERSION 4.0 SEC ID NO 17 LENGTH: 76
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Manners, John M.
APPLICANT: Marcus, John Paul
APPLICANT: Goulter, Kenneth C.
APPLICANT: Green, Jodie Lyn
TITLE OF INVENTION: ANTI-MICROBIAL PROTEIN
FILE REFERENCE: CULLN18.1CP1C1
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APPLICANT: Marcus, John Paul, APPLICANT: Goulter, Kenneth C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 17, Application US/09882434A; Patent No. US20020108144A1; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: PRT
ORGANISM: Artificial Sequence
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RESULT 6
US-09-882-434A-18
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APPLICANT: Green, Jodie Lyn
TITLE OF INVENTION: ANTI-MICROBIAL PROTEIN
FILE REFERENCE: CULLN18.1CP1C1
FURRENT APPLICATION NUMBER: US/99/882,434A
CURRENT APPLICATION NUMBER: 2001-06-15
PRIOR APPLICATION NUMBER: 09/364395
PRIOR FILING DATE: 1999-07-30
PRIOR FILING DATE: 1999-07-30
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                                                                     ; OTHER INFORMATION: M154V variant.
OTHER INFORMATION: Containing a V.
OTHER INFORMATION: from SEQ ID NO US-09-882-434A-18
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                                                                                                                                                                                                                                     PRIOR FILING DATE: 1996-01-31
NUMBER OF SEQ ID NOS: 21
SOFTWARE: FREESEQ for Windows Version 4.0
SEQ ID NO 18
LENGTH: 76
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Best Local Similarity
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PRIOR FILING DATE: 1997-01-31
PRIOR APPLICATION NUMBER: AU PN 7802
PRIOR FILING DATE: 1996-01-31
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TITLE OF INVENTION: ANTI MICROBIAL PROTEIN
FILE REPERENCE: CULLUIS 1.CPIC1
CURRENT APPLICATION NUMBER: US/09/882,434A
CURRENT FILING DATE: 2001-06-15
PRIOR APPLICATION NUMBER: 09/364395
PRIOR PILING DATE: 1999-07-30
                                                                                                                                                                                                                                                                                                                                                          PRIOR APPLICATION NUMBER: 09/117615
PRIOR FILING DATE: 1998-11-09
PRIOR APPLICATION NUMBER: PCT/AU97/00052
PRIOR FILING DATE: 1997-01-31
PRIOR APPLICATION NUMBER: AU PN 7802
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APPLICANT: Marcus, John Paul
APPLICANT: Goulter, Kenneth
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ORGANISM: Artificial Sequence FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: PRT
                                                                                                                                                                      FEATURE:
                                                                                                                                                                                          ORGANISM: Artificial Sequence
                                                                                                                                                                                                                      TYPE: PRT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                87
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ARACNPFGWKSIFIQC 102
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                                                                                            Mi54V variant. Variant MiAMP1 protein Mi54V containing a Valine at amino acid 54 (used pufrom SEQ ID NO:11 to produce).
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98.7%;
76.0%;
98.7%;
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Pred. No. 3.5e-42;
Score 419; DB 1
Pred. No. 6e-42;
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                        DB 10;
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Best Local Similarity

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US-09-882-434A-21
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               APPLICANT: Manners, John M.
APPLICANT: Marcus, John Paul
APPLICANT: Goulter, Kenneth C.
APPLICANT: Green, Jodie Lyn
TITLE OF INVENTION: ANTI-MICROBIAL PROTEIN
FILE REFERENCE: CULLN18.1CP1C1
FULE REPLICATION NUMBER: US/09/882,434A
CURRENT APPLICATION NUMBER: 09/364395
PRIOR APPLICATION NUMBER: 09/364395
PRIOR FILING DATE: 1999-07-30
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PRIOR APPLICATION NUMBER: 09/364395
PRIOR FILING DATE: 1999-07-30
PRIOR APPLICATION NUMBER: 09/117615
PRIOR FILING DATE: 1998-11-09
PRIOR FILING DATE: 1998-11-09
PRIOR APPLICATION NUMBER: PCT/AU97/00052
PRIOR FILING DATE: 1997-01-31
PRIOR APPLICATION NUMBER: AU PN 7802
PRIOR FILING DATE: 1996-01-31
PRIOR FILING DATE: 1996-01-31
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SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 21
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Patent No. US200
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APPLICANT: Green, Jodie Lyn
TITLE OF INVENTION: ANTI-MICROBIAL PROTEIN
FILE REFERENCE: CULLN18.1CP1C1
CURRENT APPLICATION NUMBER: US/09/882,434A
CURRENT FILING DATE: 2001-06-15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Manners, John M. APPLICANT: Marcus, John Paul APPLICANT: Goulter, Kenneth APPLICANT: Green, Jodie Lyn
PRIOR FILING DATE: 1999-0' PRIOR APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        OTHER INFORMATION: Mi46K/54K variant. Variant MiAMP1 protein OTHER INFORMATION: Mi46K/54K containing a Lysine at amino acid 46 and OTHER INFORMATION: a Lysine at amino acid 54.
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Similarity 97.4%;
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Pred. No. 1e-41;
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NAME/KEY: SITE
CCATION: (115)
COTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
US-09-764-868-1164
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12.5%; Score 69; DB 9; Length 1280;
Best Local Similarity 25.5%; Pred. No. 6;
Matches 25; Conservative 12; Mismatches 33; Indels 28;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 2, Application US/10044671; Patent No. US20020177147A1; Patent No. US200201771A2 No. USATION No. Maley, Karrina; APPLICANT: Mealey, Karrina; APPLICANT: Mealey, Karrina; TILE OF INVENTION: MDR1 VARIANTS AND METHODS FOR THEIR USE FILE REFERENCE: 4630-67733; CURRENT APPLICATION NUMBER: US/10/044,671; CURRENT FILING DATE: 2002-01-10; PRIOR APPLICATION NUMBER: US 60/261,578; PRIOR FILING DATE: 2001-01-12; PRIOR APPLICATION NUMBER: US 60/314,829
                                                                                                                                                                                                                      APPLICANT: Rosen et al.
TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
FILE REFERENCE: PT232
CURRENT APPLICATION NUMBER: US/09/764,868
CURRENT FILING DATE: 2001-01-17
Prior application data removed - refer to PALM or file wrapper NUMBER OF SEQ ID NOS: 1510
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 164
LENGTH: 267
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     12.8%; Score 70.5; DB 9; Length 267; 27.0%; Pred. No. 0.66; crive 13; Mismatches 36; Indels :
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     Sequence 1164, Application US/09764868
Patent No. US20020168711A1
GENERAL INFORMATION:
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SOFTWARE: PatentIn version 3.1
SEQ ID NO 2
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Best Local Similarity 27.01
Matches 20; Conservative
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ORGANISM: Canis familiaris
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: PRT
ORGANISM: Homo sapiens
                                                                                                                               US-09-764-868-1164
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US-10-044-671-2
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TITLE OF INVENTION: Methods for Improving Secondary Metabolite Production in Fungi
FILE REFERENCE: 109272.147
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                                                                                                                                                                                                                                                                                                OTHER INFORMATION: Mi46K/54V variant. Variant MiAMPI protein OTHER INFORMATION: Mi46K/54V containing a Lysine at amino acid 46 and OTHER INFORMATION: a Valine at amino acid 54.
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13.7%; Score 75.5; DB 10; Length 486;
Best Local Similarity 30.2%; Pred. No. 0.35;
Matches 29; Conservative 9; Mismatches 27; Indels 31
                                                                                                                                                                                                                                                                                                                                                                                                                        75.3%; Score 415; DB 10; Length 76; 97.4%; Pred. No. 1.8e-41; Live 1; Mismatches 1; Indels
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PRIOR FILING DATE: 1998-11-09
PRIOR APPLICATION NUMBER: PCT/AU97/00052
PRIOR PILING DATE: 1997-01-31
PRIOR FILING DATE: 1996-01-31
NUMBER OF SEQ ID NOS: 21
SOFTWARE: FastSEQ for Windows Version 4.0
LENGTH: 76
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CURRENT APPLICATION NUMBER: US/09/801,368

CURRENT FILING DATE: 2001-03-07

PRIOR APPLICATION NUMBER: US 09/487,558

PRIOR FILING DATE: 2000-01-19

PRIOR PELING DATE: 1999-10-20

PUMBER: OF SEQ ID NOS: 440
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Hecht, Peter
HOltzman, Doug
Madden, Kevin
Maxon, Mary
Milne, Todd
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ; Sequence 154, Application US/09801368; Patent No. US20020128250A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: PRT
ORGANISM: Saccharomyces cerevisiae
                                                                                                                                                                                                                                               ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                               Best Local Similarity 97.4
Matches 74; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       87 ARACNPFGWKSIFIOC 102
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   61 ARACNPEGWKSIFIQC 76
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Royer, John
Salama, Sofie
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Busby, Robert
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                           ) OTHER INFORMATION (18-09-882-434A-20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      US-09-801-368-154
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APPLICANT:
APPLICANT:
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                                                                                                                                                                                                                              TYPE: PRT
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; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-072-621-7
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CURRENT FILING DATE: 2001-08-30
PRIOR APPLICATION NUMBER: 09/584,586
PRIOR FILING DATE: 2000-05-31
PRIOR APPLICATION NUMBER: PCT/US99/11825
PRIOR APPLICATION NUMBER: 60/086,988
PRIOR FILING DATE: 1998-05-28
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Patent No. US20020169137A1
GENERAL INFORMATION:
APPLICANT: Reiner, Peter B.
APPLICANT: Connop, Bruce P.
APPLICANT: Connop, Bruce P.
APPLICANT: Pollard, Michelle
TITLE OF INVENTION: BY MODIFICATION OF AMYLOID PRECURSOR PROTEIN EXPRESSION OR ACTIVITY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 2, Application US/09866866A Patent No. US20020102244A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                               SOFTWARE: PatentIn version 3.0 SEQ ID NO 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 12.3%; Score 68; DB 9
Best Local Similarity 24.5%; Pred. No. 7.8;
Matches 24; Conservative 13; Mismatches
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CURRENT APPLICATION NUMBER: US/10/072,621
CURRENT FILING DATE: 2002-02-08
NUMBER OF SEQ ID NOS: 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Schuetz, John TITLE OF INVENTION: A Method of Identifying and/or Isolating Stem Cells FILE REFERENCE: 1340-1-021CIP2
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TYPE: PRT
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                                                          334 VFFSVLIGAFSVGQASPSIEAFANARGAAYEIFKIIDNKPSIDSYSKSGHKPDNIKGNLE 393
   60
                                                                                                                                                                                                       Local Similarity
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                                                                                                                 6 LFFSVITVMMLIAMASEMV-----NGSAFTVWSGPGCNNRAERYSKCGCSAIHQKGGYD 59
                                                                                                                                                                                                                                                                                                                                                                                       1280
                                                                                                                                                                               Conservative
                                                                                                                                                                                                       12.3%; Score 68; DB 10; Length 1280; 24.5%; Pred. No. 7.8;
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-TGQTAALYNQAGC 75
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US-10-016-634A-115
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US-09-866-866A-4
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GENERAL INFORMATION:
APPLICANT: Sorrentino, Brian
APPLICANT: Schuetz, John
APPLICANT: Schuetz, John
TITLE OF INVENTION: A Method of Identifying and/or Isolating Stem Cells
TITLE OF INVENTION: Namero US/09/866,866A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 115, Application US/10016634A Publication No. US20020192666A1 GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                      SOFTWARE: PatentIn version 3.1
SEQ ID NO 115
LENGTH: 147
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Matches 24; Conserv
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PRIOR FILING DATE: 1999-05-27
PRIOR APPLICATION NUMBER: 60/086,988
PRIOR ETILING DATE: 1998-05-28
NUMBER OF SEQ ID NOS: 27
                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Recipon, Herve
APPLICANT: Ghosh, Malavika
APPLICANT: Liu, Chenghua
TITLE OF INVENTION: Compositions and Methods Relating to Colon Specific Genes and Pro
FILE REFERENCE: DEX-0255
FULL REFERENCE: USX-0255
CURRENT APPLICATION NUMBER: USX-001-10-31
PRIOR APPLICATION NUMBER: US 60/244,258
PRIOR FILING DATE: 2000-10-31
PRIOR FILING DATE: 2000-10-31
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRIOR APPLICATION NUMBER: 09/584,586 PRIOR FILING DATE: 2000-05-31
                                                                                                                                                                                                                                                                                                                                                           NUMBER OF SEQ ID NOS: 176
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LENGTH: 1280
TYPE: PRT
ORGANISM: Homo sapiens
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  84 GSSA---RACN 91
                                                                                       32 WSGPGCNNRAER-YSKCGCSAI-----HOKGGYDFSYTGQTAALYNQAGCSGVAHTRF 83
                                                                                                                                                Local Similarity
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                                              5 WAGPGPAERAEEAVSGVGVEAKTQHAGQGAQPGGMGCGFSSGPIGMALGLGLVGTAATRG 64
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24.5%; Pred. No. 7.8;
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Pred. No. 1.7;
4; Mismatches 32;
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SUMMARIES

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thaumarin II precu probable membrane- pathogenesis-relat heat shock 18K pro hypothetical prote NADH2 dehydrogenas probable carboxype hypothetical prote	allergen - rice pathogenesis-relat env polyprotein - multidrug resistan multidrug resistan hypothetical prote allergen RA14B pre pathogenesis-relat

ALIGNMENTS

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probable aldehyde dehydrogenase - Streptomyces coelicolor (fragment)
C;Species: Streptomyces coelicolor
C;Species: O5-Nov-1999 #sequence_revision O5-Nov-1999 #text_change O5-Nov-1999
C;Accession: T35804
R,Murphy, L.; Harris, D.; Parkhill, J.; Barrell, B.G.; Rajandream, M.A.
submitted to the EMBL Data Library, August 1998
A,Reference number: Z21556
A; Molecule type: DNA
A; Residues: 1-486 <COI>A; Cross-references: EMBL: X94357; NID: g1150575; PIDN: CAA64134.1; PID: g1150586
A; Cross-references: EMBL: X94357; NID: g1150575; PIDN: CAA64134.1; PID: g1150586
A; Stachelek, C.; Stachelek, J.; Swan, J.; Botstein, D.; Konigsberg, W.
Nucleic Acids Res. 14, 945-963; 1986
Nucleic Acids Res. 14, 945-963; 1986
A; Title: Identification, cloning and sequence determination of the genes specifying hext A; Reference number: A93649; MUID: 86120382; PMID: 3003701
A; Accession: B23523
A; Molecule type: DNA
A; Residues: 1-28, 'I', 30-60, 'V', 62-196, 'S', 198-486 <STA>
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A; Residues: 1-315 < MUR>
                                                                                                                                                                                                                                                                                                                                                                                                                                                          C;Species: Saccharomyces cerevisiae
C;Date: 28-Dec-1987 #sequence revision 12-Apr-1996 #text_change 16-Jun-2000
C;Date: 28-Dec-1987 #sequence revision 12-Apr-1996 #text_change 16-Jun-2000
C;Accession: SG1608; B23523; S22430; A23958; S05731; S33656; S64279; A53632; S28555
R;Colssac, E.; Maillier, E.; Robineau, S.; Netter, P.
submitted to the EMBL Data Library, December 1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      hexokinase (EC 2.7.1.1) B - yeast (Saccharomyces cerevisiae) N;Alternate names: HEX1 protein; hexokinase II; hexokinase PII; protein G0556;
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A; Accession: S61608
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 13.7%; Score 75.5; DI Best Local Similarity 25.9%; Pred. No. 2.4; Matches 30; Conservative 20; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Genetics:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     259 DHIPIISEMPHGGYKASGFGKDMSAYSFEEYTQVKHVMFDNTAVAAK--DWHRTVF 312
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 54 Q-----KGGYDFSYTGQTAALYNQAGCSGVAHTRFGSSARACNPFGW-KSIF 99
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 MASTKLFFSVITVMML-----IAMASEMVNGSAFTVWSGPGCN-NRAERYSKCGCSAIH 53
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   T35804
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Ribelvecchio, V.G.; Kapatral, V.; Redkar, R.J.; Patra, G.; Mujer, C.; Los, T.; Ivanova, I.; Mazur, M.; Goltsman, E.; Selkov, E.; Elzer, P.H.; Hagius, S.; O'Callaghan, D.; Letess, Proc. Natl. Acad. Sci. U.S.A. 99, 443-448, 2002
A;Title: The genome sequence of the facultative intracellular pathogen Brucella melitens. A;Reference number: AD3252; PMID:11756688
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    R, Endicott, J.A.; Sarangi, F.; Ling, V. DNA Seq. 2, 89-101, 1991
A, Title: Complete CDNA sequences encoding the Chinese hamster P-glycoprotein gene family
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PIDN: AAL53581.1; PID: g17984492; GSPDB: GN00191
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C;Date: 02-Uul-1996 #sequence_revision 02-Uul-1996 #text_change 02-Feb-2001
C;Accession: 148123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          hypothetical protein C54D1.5 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 29-Oct-1999 #sequence_revision 29-Oct-1999 #text_change 18-Feb-2000
C;Accession: T28B11
R;Minx, M.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A)cross-references: GB:M60042, NID:g191168, PIDN:AAA68885.1, PID:g191169
C;Superfamily: multidrug resistance protein; ATP-binding cassette homology
C;Keywords. ATP, glycoptotein; nucleotide binding; P-loop
F;412-606/Domain: ATP-binding cassette homology <ABC1>
F;422-436/Region: nucleotide-binding motif A (P-loop)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  8; Mismatches 16; Indels 35; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                6 LFFSVITVMMLIAMASEMVN-----GSAFTVWSGPGCNNRAERYSKCGCSAIHQKGGYD 59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          29 FTVWSGPGCNNRAERYSK----CGCSAIH-----QKGGYDFSYTGQTAALYNQAGCSG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               12.6%; Score 69.5; DB 2; Length 532; 27.2%; Pred. No. 16;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A, Reference number: I48121; MUID:92135896; PMID:1685679
A, Accession: I48123
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           78 VAHTRFGSSARACNPFGWKSI 98
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A;Cross-references: GB:AE008918; I
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A, Map position: II
C, Superfamily: alcohol oxidase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             22; Conservative
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A; Residues: 1-1281 <RES>
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                  A; Accession: AB3552
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A; Accession: S64274

A; Accession: S64274

A; Accession: S64274

A; Accession: S64279

A; Accession: S64279

A; Accession: S64279

A; Residues: 1-466

A; Experimental source: strain S288C

A; Experimental source: strain S288C

B; Kriegel, Tm, Rush, J.; Vojtek, A.B.; Clifton, D.; Fraenkel, D.G.

B; Kriegel, Tm, is Rush, J.; Vojtek, A.B.; Clifton, D.; Fraenkel, D.G.

B; Kriegel, Tm, is Rush, J.; Vojtek, A.B.; Clifton, D.; Fraenkel, D.G.

B; Kriegel, Tm, S12, 148-152, 1994

A; Title: In vivo phosphorylation site of hexokinase 2 in Saccharomyces cerevisiae.

A; Recession: A55632

A; Status: preliminary

A; Moccession: A55632

A; Status: preliminary

A; Moccession: A55632

A; Status: Discretion: A; Residues: 13-21 kKB; MIPS: YGL253w

A; Genetics: A; Ge
                                                                                                                                       A; Notecule type: protein
A; Residues: 2-7; T1, 30-46; 78-111; 114-119; 166-173; 177-194; 228-236; 250-281; 283-300; 330-335
A; Residues: 2-7; T1, 30-46; 78-111; 114-119; 166-173; 177-194; 228-236; 250-281; 283-300; 330-335
Gene 36, 105-111, 1985
A; Title: The primary structure of the yeast hexokinase PII gene (HXK2) which is responsing A; Reference number: A2358
A; Reference number: A2358
A; Residues: 1-32; NV, 34-60, VV, 62-420, ST', 423-443, PH', 446-452, VV, 454-461, P', 463-486
A; Residues: 1-32; NV, 34-60, VV, 62-420, ST', 423-443, PH', 446-452, VV, 454-461, P', 463-486
A; Residues: 1-32; NV, 34-60, VV, 62-420, ST', 423-443, PH', 446-452, VV, 454-461, PV, 463-486
A; Residues: 1-32; NV, 34-60, VV, 62-420, ST', 423-443, PH', 446-452, VV, 454-461, PV, 463-486
A; Residues: 1-32; NV, 34-60, VV, 62-420, ST', 423-443, PH', 446-452, VV, 454-461, PV, 463-486
A; Residues: 1-32; NV, 34-60, VV, 62-420, ST', 423-443, PH', 446-452, VV, 454-461, PV, 463-486
A; Residues: 1-32; NV, 34-60, VV, 62-420, ST', 423-443, PH', 446-452, VV, 454-461, PV, 463-486
A; Residues: 1-32; NV, 34-60, VV, 62-420, ST', 423-443, PH', 446-452, VV, 454-461, PV, 463-486
A; Residues: 1-32; NV, 34-60, VV, 62-420, ST', 423-443, PH', 446-452, VV, 454-461, PV, 463-486
A; Residues: 1-32; NV, 34-60, VV, 62-420, ST', 423-443, PH', 446-452, VV, 454-461, PV, 463-486
A; Residues: 1-32; NV, 34-60, VV, 62-420, ST', 423-443, PH', 446-452, VV, 454-461, PV, 463-486
A; Residues: 1-32; NV, 34-60, VV, 62-420, ST', 423-443, PH', 446-452, VV, 454-461, PV, 463-486
A; Residues: 1-32; NV, 34-60, VV, 62-420, ST', 423-443, PH', 446-452, VV, 454-461, PV, 463-486
A; Residues: 1-32; NV, 34-60, VV, 62-420, ST', 423-443, PH', 446-452, VV, 454-461, PV, 463-486
A; Residues: 1-32; NV, 34-60, VV, 62-420, ST', 423-443, PH', 446-452, VV, 454-461, PV, 463-486
A; Residues: 1-32; NV, 34-60, VV, 62-420, ST', 423-443, PH', 446-452, VV, 454-461, PV, 463-486
A; Residues: 1-32; NV, 446-450, PV, 446-45
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A;Accession: $05731
A;Molecule type: protein
A;Residues: 2-12 <SCH>
R;Breitwieser, W.; Price, C.; Schuster, T.
R;Breitwieser, W.; Price, C.; Schuster, T.
A;Asat 9, 551-556, 1993
A;Title: Identification of a gene encoding a novel zinc finger protein in Saccharomyces
A;Reference number: $33654; MUID:93311123; PMID:8325518
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Best Local Similarity 30.2%; Pred. No. 3.5;
Matches 29; Conservative 9; Mismatches 27; Indels 31; Gaps
A;Cross-references: EMBL:X03483; NID:g3792; PIDN:CAA27203.1; PID:g3793
A;Note: the authors translated the codon GTT for residue 61 as Gly
A;Accession: S22430
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A.Accession: S33656
A.Molecule type: DNA
A.Residues: 1-247 <BRE>
A.Cross-references: EMBL:X67787; NID:G3707; PIDN:CAA48003.1; PID:g3710
R.Coissac, E.; Maillier, E.; Netter, P.
submitted to the Protein Sequence Database, May 1996
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                65 QTAALYNQAGCSGVAHTRF-GSSARACNP----FGW 95
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A;Cross-references: EMBL:X58723; NID:g34522; PIDN:CAA41558.1; PID:g34523 R;Chin, J.E.; Ueda, K.; Clark, D.P.; Pastan, I.; Gottesman, M.M.; Roninson, I. Cell 47, 381-389, 1986 Cell 47, 381-389, 1986 A;Title: Internal duplication and homology with bacterial transport proteins in the mdrl A;Reference number: A25059; MUID:87028230; PMID:2876781
                               A;Accession: S43838
A;Molecule type: protein
A;Residues: 656-689 <CHA>
                                                                                                                         A;Molecule type: mRNA
A;Residues: 1-184,'VV,186-1280 <CH2>
A;Residues: 1-184,'VV,186-1280 <CH2>
A;Cross-references: GB:M14758; NID:g187468; PIDN:AAA59575.1; PID:g307180
A;Cross-references: GB:M14758; NID:g187468; PIDN:AAA59575.1; PID:g307180
B;Chambers, T.C.; Pohl, J.; Glass, D.B.; Kuo, J.F.
Biochem. J. 29; 309-215, 1994
A;Telle: Phosphorylation by protein kinase C and cyclic AMP-dependent protein kinase
A;Reference number: S43838; MUID:94220047; PMID:7909431
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A; Molecule type: DNA
A; Residues: 1-22, 'R' <KI2>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A;Description: Transcriptional regulation of multidrug resistance gene (MDR1) expression A;Reference number: $15500
A;Accession: $15500
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A;Molecule type: DNA
A;Residues: 1-1280 «CHE»
A;Cross-references: GB:M29447; GB:J05168; NID:g187496; PIDN:AAA59576.1; PID:g386862
R;Kioke, N.; Yamano, Y.; Komano, T.; Ueda, K.
submitted to JIPID, April 1991
A;Reference number: PS0162
A;Accession: PS0162
R;Gekeler, V.; Weger, S.; Probst, H.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A;MoLecule type: DNA
A;Residues: 1-2</TO>
R;Kioka, N.; Yamano, Y.; Komano, T.; Ueda, K.
Bubmitted to the EMBL Data Library, April 1991
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           multidrug resistance protein 1 - human

N;Alternate names: P-glycoprotein 1

C;Species: Homo sapiens (man)

C;Date: 31-Dec-190 #sequence revision 18-Aug-1995 #text_change 19-Jan-2001

C;Accession: A34914; PS0166; $15500; A25059; S43838; I52238; I65204

R;Chen, C.; Clark, D.; Ueda, K.; Pastan, I.; Gottesman, M.M.; Roninson, I.B.

J. Biol. Chem. 265, 506-514, 1990

A;Title: Genomic organization of the human multidrug resistance (MDR1) gene and origin
A;Reference number: A34914; MUID:90094448; PMID:1967175
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A;Introns: 84/3; 127/1; 166/2; 271/2; 331/1; 392/3; 433/2; 585/2; 1089/1; 1530/3
C;Superfamily: laminin beta-1 chain; laminin-type EGF-like homology
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A;Molectie type: DNA
A;Residues: 1-1557 <MIN>
A;Residues: 1-1557 <MIN>
A;Cross-references: EMBL:U46673; PIDN:AAC48152.1; GSPDB:GN00028; CESP:C54D1.5
A;Experimental source: strain Bristol N2; clone C54D1
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A;Description: The sequence of C. elegans cosmid C54D1.
A;Reference number: Z20527
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Pred. No. 55
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F;638-708/Domain: linker <LINS
F;709-993/Domain: linker <LINS
F;709-993/Domain: hydrophobic <HB2>
F;909-993/Domain: hydrophobic <HB2>
F;909-1280/Domain: hydrophobic <HB2>
F;1053-1249/Domain: ATP-binding cassette homology <ABC2>
F;1070-1077/Region: nucleotide-binding motif A (P-loop)
F;1196-1200/Region: nucleotide-binding motif B
F;91,94-99/Binding site: carbohydrate (Asn) (covalent) #status predicted
F;433/Binding site: ATP (Lys) #status predicted
F;433/Binding site: Dosphate (Ser) (covalent) (by protein kinase C) #status expected (Ser) (for a status of the status of th
A; Introns: 25/2; 66/1; 114/2
                                                       A;Gene: CESP:F12A10.1
                                                                                                                              A;Cross-references: EMBL:U28731; NID:g861241; PID:g861242; PIDN:AAA68294.1; CESP:F12A10.
A;Experimental source: strain Bristol N2
                                                                                                                                                                                                                                            A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-184 <GEI5
                                                                                                                                                                                                                                                                                                                                                                                                                            A;Reference number: Z18451
A;Accession: T16044
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A:Description: The sequence of C. elegans cos
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             R;Geisel
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A; Residues: 800-856 < RE2>
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A;Title: mdr1/P-glycoprotein gene segments analyzed from various human leukemic cell li, A;Reference number: I52238; MUID:90290529; PMID:1972623
A;Accession: I52238
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A; Residues: 178-215 < RES>
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Query Match

12.3%;

Score 67.5;

DB 2;

Length 184;

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C;Species: Salmonella enteritidis
C;Species: Salmonella enteritidis
C;Date: 31-Dec-1996 #sequence_revision 31-Dec-1996 #text_change 08-Oct-1999
C;Accession: 076640
B;Collinson, S.K.; Clouthier, S.C.; Doran, J.L.; Banser, P.A.; Kay, W.W.
J. Bacteriol. 178, 662-667, 1996
A;Title: Salmonella enteritidis agfBAC operon encoding thin, aggregative fimbriae.
A;Recence number: 076039; MUID:96146512; PMID:8550497
A;Accession: JC6040
A;Recession: JC6040
A;R
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Note: fimbriae bind to fibronectin, plasminogen, tissue plasminogen activator
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  proceinase inhibitor - rice

proceinase inhibitor - rice
() Species: Oryza sativa (rice)
() Date: 24-Mar-1999 #sequence_revision 24-Mar-1999 #text_change 09-Jun-2000
() Date: 24-Mar-1999 #sequence_revision 24-Mar-1999 #text_change 09-Jun-2000
() Accession: T02667
() H.; Park, J.H.; Lee, G.R.
() Ryvun, C.H.; Lee, J.H.; Park, J.H.; Lee, G.R.
() Ryvun, C.H.; Lee, J.H.; Park, J.H.; Lee, G.R.
() Ryvun, C.H.; Lee, J.H.; Park, J.H.; Lee, G.R.
() Ryvun, T02667
() Ryvun, Tanslated from GB/EMBL/DDBJ
() Ryvun, Tanslated from GB/EMBL/DDBJ
() Ryvun, T.M.
() Ryvun, T.M
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12.1%; Score 66.5; DB 2; Length 151;
Best Local Similarity 31.0%; Pred. No. 10;
Matches 18; Conservative 11; Mismatches 16; Indels 13; Gaps
                                                                                                                                                                                                              2 ASTKLFFSVITVMMLIAMASEMVNGSAFTVWSGPGCNNRAERYS-----KCGCSAIHQKG 56
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                                                Gaps
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F;1-21/Domain: signal sequence #status predicted <SIG>
F;22-151/Product: fimbrin protein agfB #status predicted <MAT>
                                                                                                                                                                                                                                                                                                                                                                                                                                                             138 -----GYSGYG-----GAYPGMYGGGMGGSYGSSSWGSYSSSRSG 172
                                                34; Indels
                                                                                                                                                                                                                                                                                                                                                                 37 CNNRAERYSKCGCSAIHQKGGYDFSYTGQTAALYNQAGCSGVAHTRFG
     Pred. No. 9.6;
                                                      11; Mismatches
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     24.18;
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hes 19; Conservative
                                                           26, Conservative
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A,Introns: 21/1
C,Superfamily: gamma-thionin
Best Local Similarity
Matches 26, Conserva
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Matches
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A,Molecule type: mRNA
A,Residues: 1-162 <NAK>
A,Cross-treferences: EMBL:X66257; NID:9311892; PIDN:CAA46983.1; PID:9311893
C;Comment: This protein shows a sequence similarity to alpha-amylase/trypain inhibitor f.
C;Superfamily: wheat alpha-amylase inhibitor
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Cispecies: Oryaa sativa (rice)
Cjate: 30-Sep-1993 #sequence revision 30-Sep-1993 #text_change 20-Jun-2000
Cjate: 30-Sep-1993 #sequence revision 30-Sep-1993 #text_change 20-Jun-2000
Cjacession: 521157; JG4887; S31079
R;Izumi, H.; Adachi, T.; Fujii, N.; Matsuda, T.; Nakamura, R.; Tanaka, K.; Urisu, A.; Ku:
R;Izumi, H.; Adachi, 1992
A;Itile: Nuclectide sequence of a cDNA clone encoding a major allergenic protein in rice
A;Reference number: S21157; MUID:92289999; PMID:1376283
                                                                                                                                                                                                                                                                                                                                            Cjāccession: $31078
Rjādachi, T.; Izumi, H.; Yamada, T.; Tanaka, K.; Takeuchi, S.; Nakamura, R.; Matsuda, T.
Rjādachi, T.; Izumi, H.; Yamada, T.; Tanaka, K.; Takeuchi, S.; Nakamura, R.; Matsuda, T.
Ajant Mol. Biol. 21, 239-248, 1993
Ajatiche: Gene structure and expression of rice seed allergenic proteins belonging to the Ajaterence number: S31078; MUID:93144699; PMID:7678765
Ajaccession: S31078.
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A;Title: Rice allergenic protein and molecular-genetic approach for hypoallergenic rice.
A;Reference number: JC4887; MUID:97141195; PMID:8987539
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                                                                                                                                                                                                                                         seed allergen RA5 - rice
C,Species: Oryza sativa (rice)
C,Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 20-Jun-2000
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A;Cross-references: EMBL:D11431; NID:g218194; PIDN:BAA01997.1; PID:g218195
R;Nakamura, R.; Matsuda, T.
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12.1%; Score 66.5; DB 2; Length 162;
1 Similarity 21.5%; Pred. No. 11;
31; Conservative 17; Mismatches 37; Indels 59; Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A;Cross-references: EMBL:D11430; NID:g218196; PIDN:BAA01996.1; PID:g218197 C;Superfamily: wheat alpha-amylase inhibitor C;Keywords: seed
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                                   87
30 TVWSGPGCNNRAERYSKCGCSAIHQKGGYDFSYTGQTAALYNQAGCSGVAHTRFGSSA
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A,Status: nucleic acid sequence not shown
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A; Residues: 1-157 <ADA>
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A; Molecule type: mRNA
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C;Keywords:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               R;Parkhill, J.; Wren, B.W.; Thomson, N.R.; Titball, R.W.; Holden, M.T.G.; Prentice, M.B. deno-Tarrage, A.M.; Chillingworth, T.; Cronin, A.; Davies, R.M.; Davis, P.; Dougan, G.; il, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.; Whitehead, S.; Barrell, Nature 413, 523-527, 2001
                                                                                                                                                                                                                                                                                                                                                                                 A;Gene: nuoF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A; Molecule type: DNA
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R;Saunders, D.C.; Harris, D.; Bentley, S.D.; Parkhill, J.; Barrell, B.G.; Rajandream, submitted to the EMBL Data Library, December 1998
A;Reference number: Z21552
A;Reference number: Z21552
A;Reference number: Z21552
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A; Gene: SCOEDB: SC1A9.07
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A; Residues: 1-251 <SAU>
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                                                                                                                                                                                                                                                                   Query Match
                                                                                                                                                                                                                                                                                                                             Superfamily: NADH dehydrogenase (ubiquinone) chain F; NADH dehydrogenase (ubiquinone)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Status: preliminary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ;Title: Genome sequence of Yersinia pestis, the causative agent of plague;Reference number: AB0001; MUID:21470413; PMID:11586360
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ;Species: Yersinia pestis
;Date: 02-Nov-2001 #sequence_revision 02-Nov-2001 #text_change 03-Jun-2002
;Accession: AE0311
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Cross-references: EMBL:AL034446; PIDN:CAA22377.1; GSPDB:GN00070; SCOEDB:SC1A9.07;
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                                                                                   216 VWGKPTCVNNVE--TLCNVPAIIEHGVE--WYQGITAGKSNDAGTK-----LMGFSGRVK 266
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              194 PAG-PGLAH 201
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                                                   91 NPFGWKSIF 99
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th, T.; Connerton, P.; Cronin, A.; Davis, P.; Davies, R.M.; Dowd, L.; White, N.; Farrar, S.; Moule, S.; O'Gaora, P.
Nature 413, 848-852, 2001
A;Authors: Parry, C.; Quail, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.; A;Title: Complete genome sequence of a multiple drug resistant Salmonella enterica sero, A;Reference number: AB0502; PMID:11677608
                                                                                                                                                                                           nucleation component of curlin monomers [imported] - Salmonella enterica subsp. enterica C;Species: Salmonella enterica subsp. enterica serovar Typhi A;Note: this species has also been called Salmonella typhi C;Date: 09-Nov-2001 #sequence_revision 09-Nov-2001 #text_change 09-Nov-2001 C;Accession: AH0635
                                                                                                                                          R; Parkhill, J.; Dougan, G.; James, K.D.; Thomson, N.R.; Pickard, D.; Wain, J.; th. T.; Connerton, P.; Cronin, A.; Davis, P.; Davies, R.M.; Dowd, L.; White, N.
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A;Gene: mdr2
C;Superfamily: multidrug resistance protein; ATP-binding cassette homology C;Keywords: ATP; duplication; glycoprotein; nucleotide binding; P-loop; tr: F;1-637,653-1276/Region; duplication
RESULT 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      F;1049-1245/Domain: ATP-binding cassette homology <ABC2>
F;1067-1074/Region: nucleotide-binding motif A (P-loop)
F;1197-1196/Region: nucleotide-binding motif B
F;88,94/Binding site: carbohydrate (Asn) (covalent) #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     F;409-603/Domain: ATP-binding cassette homology <ABC1>F;426-433/Region: nucleotide-binding motif A (P-loop)F;550-554/Region: nucleotide-binding motif B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A;Note: the nucleotide sequence was submitted to the EMBL Data Library, January 1996 C;Comment: This is an integral membrane protein overproduced in multidrug-resistant cell tructurally and functionally unrelated lipophilic antitumor drugs.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    R;Kirschner, L.S.

Nucleic Acids Res. 24, 2829-2834, 1996

A;Title: De novo generation of simple sequence during gene amplification.

A;Reference number: S70711; MUID:96313253; PMID:8759018
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        C;Species: Mus musculus (house mouse)
C;Date: 31-Dec-1990 #sequence revision 31-Dec-1990 #text_change 19-Jan-2001
C;Accession: A30409; S70711
R;Gros, P.; Raymond, M.; Bell, J.; Housman, D.
Mol. Cell. Biol. 8, 2770-2778, 1988
A;Title: Cloning and characterization of a second member of the mouse mdr gene family.
A;Reference number: A30409; MUID:88302195; PMID:3405218
A;Accession: A30409; MUID:88302195; PMID:3405218
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                C;Genetics
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A;Cross-references: EMBL:U46839; NID:g1228142; PIDN:AAC52722.1; PID:g1228143
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A; Molecule type: DNA
A; Residues: 43-92 < KIR>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A; Status: nucleic acid sequence not shown; translation not shown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A;Cross-references: GB:J03398; NID:g199109; PIDN:AAA39516.1; PID:g387428
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A; Molecule type: mRNA
A; Residues: 1-1276 < HSU>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ;1072/Binding site: ATP (Lys) #status predicted
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                                                                                                                                            60 FS-----YTGQTAALYNQAGC 75
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Churcher

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A;Accession: AH0635
A;Status: preliminary
A;Wolecule type: DNA
A;Residues: 1-151 <PAR>
A;Cessereferences: GB;AL513382; PIDN:CAD08267.1; PID;g16502314; GSPDB:GN00176
C;Genetics:
A;Gene: STY1180
                                                                                                                                           Query Match
Best Local Similarity 31.0%; Pred. No. 13;
Matches 18; Conservative 11; Mismatches 16; Indels 13; Gaps
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Search completed: January 12, 2003, 09:39:24 Job time : 45 secs

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Maximum Match 100%
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Copyright (c) 1993 - 2003 Compugen Ltd
  AMP1 MACIN
HXKB YEAST
PGK CHLMU
MDR3 CRIGR
LML1 CAEEL
MDR1 HUMAN
VEF GVHA
CSGB SALTY
RAO5 ORYSA
RA17 ORYSA
MDR2 MOUSE
CSGB SALTI
OSL3 ARATH
ORYSA
HXKA YEAST
LFC_CARRO
LFC_TACTR
PRO4_LYCES
MDA3_HUMAN
EXR1_THADA
EXR1_AATH
AT11_LYCES
CRYP_CRYPA
PRO6_LYCES
CRYP_CRYPA
HS6C_DROME
YEL2_YEAST1
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MRKC KLEPN
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7 rhizobium s
7 klebsiella
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RESULT 2 HXKB_YEAST

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SEQUENCE OF 1-18, AND PHOSPHORYLATION OF SER-14.

MEDIAINE=98384167; PubMed=9718324;

Behlke J., Heidrich K., Naumann M., Mueller E.-C., Otto A., Reuter R.,

Kriegel T.;

Kriegel T.;

Hexokinase 2 from Saccharomyces cerevisiae: regulation of oligomeric
structure by in vivo phosphorylation at serine-14.";
                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
MEDLINE-86056943; PubMed=3905511;
Froehlich K.-U., Entian K.-D., Mecke D.;
"The primary structure of the yeast hexokinase PII gene (HXK2) which in responsible for glucose repression.";
Gene 36:105-111(1985).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE OF 118-126; 175-184 AND 303-313.
SEQUENCE 05 38531 / Y41;
MEDLINE=95255188; PubMed=7737086;
Morbeck J., Blomberg A.;
"Gene linkage of two-dimensional polyacrylamide gel electrophoresis resolved proteins from isogene families in Saccharomyces cerevisiae by microsequencing of in-gel trypsin generated peptides.";
Electrophoresis 16:149-156(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PHOSPHORYLATION OF SER-157.
MEDLINE-97199316; PubMed-9047292;
Heidrich K., Otto A., Behlke J., Rush J., Wenzel K.W., Kriegel T.;
"Autophosphorylation-inactivation site of hexokinase 2 in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STRAIN=W303;
MEDLINE=93311123; PubMed=8322518;
Breitwieser W., Price C., Schuster T.;
Identification of a gene encoding a novel zinc finger protein in Saccharomyces cerevisiae.";
Yeast 9:551-556(1993).
                                                                                                                                                                                                            SEQUENCE FROM N.A.
MEDLINE=86120382; PubMed=3003701;
Stachelek C., Stachelek J., Swan J., Botstein D., Konigsberg W.;
"Identification, cloning and sequence determination of the genes
specifying hexokinase A and B from yeast.";
Nucleic Acids Res. 14:945-963(1986).
                                                                                                                   Saccharomyces cerevisiae (Baker's yeast).

Bukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes; Saccharomycetales; Saccharomycetaceae; Saccharomycetales.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PHGSPHORYLATION OF SER-14.
MEDINE=9414477; Pubmed=8286332;
Kriegel T.M., Vojtek A.B., Clifton D., Fraenkel D.G.;
Kriegel T.M., Vojtek A.B., Clifton D., Fraenkel D.G.;
In vivo phosphorylation site of hexokinase 2 in Saccharomyces
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDLINE-97127827; PubMed=8972578; Coissac E., Maillier E., Robineau S., Netter P.; Sequence of a 39,411 bp DNA fragment covering the left end of chromosome VII of Saccharomyces cerevisiae.";
                          30-MAY-2000 (Rel. 39, Last sequence update)
30-MAY-2000 (Rel. 39, Last sequence update)
30-MAY-2000 (Rel. 39, Last annotation update)
HO-MAY-2000 (Rel. 39, Last annotation update)
HACKINGS B (EC 2.7.1.1) (HACKINGSE PII).
485 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Biochemistry 36:1960-1964(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Biochemistry 33:148-152(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE OF 1-246 FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Yeast 12:1555-1562(1996).
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 STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
STRAIN=S288c / FY1679;
                                                                                                                                                                                  NCBI_TaxID=4932;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       cerevisiae
   HXKB YEAST
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                                                                                           -i- CATALYTIC ACTIVITY: ATP + D-hexOBE = ADP + D-hexOBE 6-phosphate.
                                                                                                                 Anderson C.M., Stenkamp R.E., Steitz T.A.;
"Sequencing a protein by X-ray crystallography. II. Refinement of yeast hexokinase B co-ordinates and sequence at 2.1-A resolution.";
J. Mol. Biol. 123:15-33(1978)
-!- FUNCTION: MAIN GLUCOSE PHOSPHORYLATING ENZYME, MAY PLAY A REGULATORY ROLE IN BOTH INDUCTION AND REPRESSION OF GENE EXPRESSION BY GLUCOSE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Transferase; Kinase; Glycolysis; Allosteric enzyme; ATP-binding; 3D-structure; Phosphorylation.

INIT MET 0 0 0 BINDING 110 110 ATP (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ATP (BY SIMILARITY),
GLUCOSE-BINDING (POTENTIAL)
PHOSPHORYLATION.
PHOSPHORYLATION.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            N -> I (IN REF. 1).
I -> N (IN REF. 2).
G -> V (IN REF. 1).
T -> S (IN REF. 1).
YN -> ST (IN REF. 2).
TS -> PH (IN REF. 2).
I -> V (IN REF. 2).
A -> P (IN REF. 2).
X-RAY CRYSTALLOGRAPHY (2.1 ANGSTROMS).
                                                                                                                                                                                                                                                                                                                                 EMBL; X6775; CAA96973.1; -
EMBL; X67787; CAA48003.1; -
EMBL; X67787; CAA48003.1; -
EMBL; 328555; S28555.
PIR; S28555; S28555.
PIR; PF001322; HXK2.
PFam; PF003122; HXK2.
PFAm; PF003177; hexokinase; 1.
PROPINTS; PRO0415; HEXOKINASE.
PRODOM; PD001109; HEXOKINASES; 1.
             MEDLINE=78244654; PubMed=355643;
                                                                                                                                                                                                                                                                                                   EMBL; X03483; CAA27203.1; -. EMBL; M11181; AAA34697.1; -. EMBL; X94357; CAA4134.1; -. EMBL; Z7275; CAA96973.1; -. EMBL; X67787; CAA48003.1; -.
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Matches 29
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Q9PLN4;
16-OCT-2001
            SEQUENCE FROM N.A.

STRAIN-MOPN / Nigg;

MEDLINE=20150255; PubMed=10684935;

Read T.D., Brunham R.C., Shen C., Gill S.R., Heidelberg J.F.,

White O., Hickey E.K., Peterson J., Utterback T., Berry K., Ba

Linher K., Weidman J., Khouri H., Craven B., Bowman C., Dodson

Gwinn M., Nelson W., DeBoy R., Kolonay J., McClarty G., Salzber

Elsen J., Fraser C.M.,

"Genome Bennences of Chlamydia trachomatic McDm and Chlamydia

"Genome Bennences of Chlamydia trachomatic McDm and Chlamydia
                                                                                                                 16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Phosphoglycerate kinase (EC 2.7.2.3).
PK OR TC0065.
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                                                                                                  Chlamydia muridarum.
Bacteria; Chlamydiales;
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                                                                                         NCBI_TaxID=83560;
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"Genome sequences of Chlamydia trachomatis MoPn and pneumoniae AR39.";
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                                                                                                                                                                                                                                                                                       Similarity
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                                                                                                                                                                     STANDARD;
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                                                                                                  Chlamydiaceae; Chlamydia
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Pred. No. 1;
9; Mismatches 27;
                                                                                                                                                                     PRT;
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                                                                                                                                                                     403 AA.
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                                                                                                                                                                                                                                                                                               Length 485;
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       Chlamydia
                       Salzberg
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                              Bass S.,
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Pfam; PF00162; PGK; 1.

PRINTS: PRO0477; PHGLYCKINASE.

PROSITE; PS00111; PGLYCERATE_KINASE; 1.

PROSITE; PS00111; PGLYCERATE_KOMPLETE proteome.

Transferase; Kinase; Glycolysis; Complete proteome.

Transferase; Kinase; Glycolysis; Complete proteome.

Transferase; Kinase; Glycolysis; TA80C7A550D89F64 CRC64;

TRANSFERMENT PROVINCE PROVINCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MDR3_CRIGR STANDARD; PRT; 1281 AA. P23174; PRT) (Rel. 20, Created) 01-NOV-1991 (Rel. 20, Last sequence update) 16-OCT-2001 (Rel. 40, Last annotation update) 16-OCT-2001 (Rel. 40, Last annotation update)
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                                                                                                                                                                                                                                               -!- FUNCTION: ENERGY-DEPENDENT EFFLUX PUMP RESPONSIBLE FOR DECI-
DRUG ACCUMULATION IN MULTIDRUG-RESISTANT CELLS.
-!- SUBSCELLULAR LOCATION: Integral membrane protein.
-!- MISCELLANEOUS: PGP ISOFORMS DIFFER IN THEIR DRUG TRANSPORT
CAPABILITIES: PGP1 AND PGP2 CAN MEDIATE MDR, WHILE PGP3 API
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        This SWISS-PROT entry is copyright. It is produced through a collab between the Swiss Institute of Bioinformatics and the EMBL outst the European Bioinformatics Institute. There are no restrictions use by non-profit institutions as long as its content is in modified and this statement is not removed. Usage by and for comentities requires a license agreement (See http://www.isb-sib.ch/an
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.

MEDLINE=92135896; PubMed=1685679;
Endicott J.A., Sarangi F., Ling V.;
"Complete cDNA sequences encoding the Chinese hamster P-glycoprotein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EMBL; AE002274; AAF73528.1; -. HSSP; P36204; 1VPE. TIGR; TC0065; -.
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-!- CATALYTIC ACTIVITY: ATP + 3-phospho-D-glycerate = phospho-D-glyceroyl phosphate.
-!- PATHWAY: Second phase of glycolysis; second step.
-!- SUBUNIT: MONOMER (BY SIMILARITY).
-!- SUBCELLULAR LOCATION: Cytoplasmic (By similarity)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Cricetinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Cricetulus griseus (Chinese hamster)
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PGY3 OR PGP3.
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                                                                                                                                                                                                                                                                                                                                                                                                                      DNA Seq.
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-!- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).
-!- SIMILARITY: BELONGS TO THE PHOSPHOGLYCERATE KINASE FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 361 AAVVALAGCTSQISHVSTGGGA 382
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                                                                                                                                                                                          SIMILARITY: BELONGS TO THE ABC TRANSPORTER FAMILY. MDR SUBFAMILY.
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                                                                                                                                                                                                                                                                                                                                                                                                      family.";
Seq. 2:89-101(1991).
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Pred. No. 2.
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(See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
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Rhabditidae; Peloderinae; Caenorhabditis.
NCBI_TaxID=6239;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          6 LFFSVITVMMLIAMASEMVN-----GSAFTVWSGPGCNNRAERYSKCGCSAIHQKGGYD 59
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R InterPro; IPR003439; ABC_transportr.
InterPro; IPR003439; ABC_transportr.
R Pfam; PF000065; ABC_transportr.
R Pfam; PF000066; ABC_transportr; 2.
R Probom; P000066; ABC_transportr; 2.
R Probom; P000066; ABC_transportr; 2.
R PROSITE; PS00211; ABC_TRANSPORTER; 1.
R ATP-binding; Glycoprotein; Transmembrane; Transmembrane; 2.
T TRANSMEM SB 78 POTENTIAL.
T TRANSMEM 12 79 POTENTIAL.
T TRANSMEM 12 142 POTENTIAL.
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                                                                                                                                                                                                                                                                                                                                                                                                                         Score 69; DB 1; Length 1281; Pred. No. 12;
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                                                                                                                                                                                                                                                                                                                                                                                                   2203EF61EBB29602 CRC64;
                                                                                                                                                                                                                                                                          CYTOPLASMIC (POTENTIAL) POTENTIAL.
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ATP (POTENTIAL)
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01-NOV-1997 (Rel. 35, Last sequence update)
01-NOV-1997 (Rel. 35, Last annotation update)
Laminin-like protein C54D1.5 precursor.
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LAMININ EGF-LIKE 2.
LAMININ EGF-LIKE 3.
LAMININ EGF-LIKE 4.
LAMININ EGF-LIKE 5 (N-TERMINAL).
LAMININ EGF-LIKE 5 (C-TERMINAL).
LAMININ EGF-LIKE 6 (INCOMPLETE).
LAMININ EGF-LIKE 9.
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MEDIJNE=97190336; PubMed=9038218;
Chen G., Duran G.E., Steger K.A.,
Dumontet C., Sikic B.I.;
"Multidrug-resistant human sarcom
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MDR1 HUMAN STANDARD; PRT; 1280 AA.

P08183; Q12755; Q14812;
01-AUG-1988 (Rel. 08, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Multidrug resistance protein 1 (P-glycoprotein 1) (CD
ABCB1 OR PGY1 OR MDR1.
HOmo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; E
Mammalla; Eutheria; Primates; Catarrhini; Hominidae;
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MEDLINE=90094448; PubMed=1967175;
Chen C.-J., Clark D.P., Ueda K.,
                                                                                                                                                                                             Roninson I.B.;
"Genomic organization of the human and origin of P-glycoproteins.";
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Chen C.-J., Chin J.E., Ueda K., Clark D.P.,
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                                                                                                                                                                                   Biol. Chem.
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                                                rug-resistant human sarcoma cells with a mutant P-glycoprotein, phenotype, and resistance to cyclosporins.";
. Chem. 272:5974-5982(1997).
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Gibson A.;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Higuchi S., Nakamura Y.; "Three hundred twenty-six genetic variations in genes encoding nine members of ATP-binding cassette, subfamily B (ABCB/MDR/TAP), in the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDIINE=90290529; PubMed=1972623;
Gekeler V., Weger S., Probst H.;
"mdri/P-glycoprotein gene segments analyzed from various human
leukemic cell lines exhibiting different multidrug resistance
                                                                                                                                                                                                                                                   EMBL;
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-!- FUNCTION: ENERGY-DEPENDENT EFFLUX PUMP RESPONSIBLE
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Saito S., Iida A., Sekine A., Miura Y.,
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Submitted (JUL-1991) to the EMBL/GenBank/DDBJ databases
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                                                                                                                                           L; M14758; AAA59575.1; M29424; AAA59576.1; J W29425; AAA59576.1; J W29427; AAA59576.1; J W29427; AAA59576.1; J W29428; AAA59576.1; J W29428; AAA59576.1; J W29431; AAA59576.1; J W29431; AAA59576.1; J W29432; AAA59576.1; J W29432; AAA59576.1; J W29433; AAA59576.1; J W29434; AAA59576.1; J W29434; AAA59576.1; J W29438; AAA59576.1; J W29444; J W
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             A25059;
A34914;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DATABASE: NAME=Atlas Genet. Cytogenet. Oncol. Haematol.; WWW="http://www.infobiogen.fr/services/chromcancer/Genes/PGY1ID105.html".
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AF016535; AAB69423.:
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Roelvink P.W., Corsaro B.G., Granados R.R.; "Characterization of the Helicoverpa armigera and Pseudaletia
MEDLINE=96068802; PubMed=7595376;
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Viruses; dsDNA viruses, no RNA stage; Baculoviridae; Granulovirus.
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N-LINKED (GLCNAC. .) (POTENTIAL)
N-LINKED (GLCNAC. .) (POTENTIAL)
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01-0CT-1996 (Rel. 34, Last sequence update)
15-DEC-1998 (Rel. 37, Last pennotation update)
viral enhancing factor (VEF) (Enhancin) (104 kDa glycoprotein)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Heliothis armigera granulosis virus (HaGV) (Heliothis armigera
                                                                                                                                                                                      PROSITE; PS00211; ABC TRANSPORTER; 2.
ATP-binding; Glycoprotein; Transmembrane; Transport; Repeat;
Multigene family; Polymorphism.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 68; DB 1; Length 1280;
Pred. No. 15;
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A -> S (IN DBSNP:2032582).
/FTId=VAR_013361.
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G -> V (IN REF. 1 AND 3).

MISSING (IN REF. 3).

G -> A (IN REF. 3).

Q -> S (IN REF. 3).
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(BY SIMILARITY).
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                   InterPro; IPR003593; AAA ATPase.
InterPro; IPR003439; ABC_transportr.
InterPro; IPR001140; ABCCranprtrTM.
                                                                                        Pfam; PF00005; ABC_tran; 2.
Pfam; PF0064; ABC_membrane; 2.
ProDom; PD000006; ABC_transportr; 2.
SMART; SM00382; AAA; 2.
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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MEDLINE=98117058; PubMed=9457880;
Romling U., Bian Z., Hammar M., Sierralta W.D., Normark S.;
"Curli fibers are highly conserved between Salmonella typhimurium and Escherichia coli with respect to operon structure and regulation.";
J. Bacteriol. 180:722-731(1998).
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MEDLINE=21534948; PubMed=11677609,
McClelland M., Sanderson K.E., Spieth J., Clifton S.W., Latreille P.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          213 GGAYYGAFWTAPASTNLGEYLRVSPTNWMVIHELGHAYDFVFTVNTRLIEIWNNSFCDRI 272
unipuncta granulovirus enhancin genes.";
J. Gen. Virol. 76:2863-2705(1995).
-!- FUNCTION: INVOLVED IN DISRUPTION OF THE PERITROPHIC MEMBRANE AND FUSION OF NUCLECCAPELES WITH MIDGUT CELLS (BY SIMILARITY).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (POTENTIAL)
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01-OCT-1996 (Rel. 34, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Minor curlin subunit precursor (Fimbrin SEF17 minor subunit)
CSGB OR AGFB OR STM1143.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DB 1; Length 902;
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(GLCNAC...)
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Pfam; PF03272; Enhancin; 1.
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28.6%;
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MEDLINE-93144699; PubMed=7678765;
Adachi T., Izumi H., Yamada T., Tanaka K., Takeuchi S.,
Adachi T., Izumi H., Yamada T., Tanaka K., Takeuchi S.,
Nakamura R., Matsuda T.,
"Gene etructure and expression of rice seed allergenic proteins
belonging to the alpha-amylase/trypsin inhibitor family.";
belonging to the alpha-amylase/trypsin inhibitor family.";
Plant Mol. Biol. 21:239-248(1993).
-I- PTM: FIVE DISULFIDE BONDS ARE PRESENT (BY SIMILARITY).
-I- SIMILARITY: BELONGS TO THE CEREAL TRYPSIN/ALPHA-AMYLASE INH:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      01-JUN-1994 (Rel. 29, Created)
01-JUN-1994 (Rel. 29, Last sequence update)
01-JUN-1994 (Rel. 29, Last annotation updat
                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzeae; Oryza.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SPECIES-S.enteritidis; STRAIN=27655-3B;
MEDLINE=96146512; PubMed=8550497;
Collinson S.K., Clouthier S.C., Doran J.L., Banser P.A., Kay W.W.;
"Salmonella enteritidis agfBAC operon encoding thin, aggregative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Oryza sativa (Rice).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Q01881;
01-JUN-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EMBL; U43280; AAC43598.1; -. StyGene; SG10609; csgB.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                  NCBI_TaxID=4530;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Seed allergenic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Fimbria; Signal; Complete proteome SIGNAL 1 21 POTEN'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   J. Bacteriol. 178:662-667(1996).
-I- FUNCTION: CURLIN IS THE STRUCTURAL SUBUNIT OF THE CURLI.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Waterston R., Wilson R.K.;
"Complete genome sequence of Salmonella enterica serovar Typhimurium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               timbriae."
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      69 SVISQEGGNNRAK------VDQAGNYNFAYIEQT----GNANDASISQSAYGNSA 113
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     30 TVWSGPGCNNRAERYSKCGCSAIHQKGGYDFSYTGQTAALYNQAGCSGVAHTRFGSSA
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MINOR CURLIN SUBUNIT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    157 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      update)
         TRYPSIN/ALPHA-AMYLASE INHIBITOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DB 1;
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N., Mulvaney E.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 13;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AT GROWTH
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RESULT 10
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Best Local :
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Q01883;
"Nucleotide sequence of a cDNA clone encoding a major allergenic protein in rice seeds. Homology of the deduced amino acid sequenwith members of alpha-amylase/trypsin inhibitor family.";
                                                                                    MEDLINE=92289999; PubMed=1376283;
Izumi H., Adachi T., Fujii N., Matsuda T., Nakamura R., Tanaka K.,
Urisu A., Kurosawa Y.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              01-JUN-1994 (Rel. 29, Created)
01-JUN-1994 (Rel. 29, Last sequence update)
01-JUN-1994 (Rel. 29, Last annotation updat
Seed allergenic protein RA17 precursor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Spermartoideae; Oryzeae; Oryza.
                                                                                                                                                                                                                SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                   "Gene structure and expression of rice seed allergenic proteins belonging to the alpha-amylase/trypsin inhibitor family."; Plant Mol. Biol. 21:239-248(1993).
                                                                                                                                                                                                                                                                                                                                                                 TISSUE=Seeq;
MEDLINE=93144699; PubMed=7678765;
MEDLINE=93144699; PubMed=7678765;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Oryza sativa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ORYSA
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                                                                                                                                                                                                                                                                                                                                                  Nakamura R., Matsuda T.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
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22.1%;
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Pred. No. 3
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         e deduced amino acid sequence
inhibitor family.";
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         7
FEBS Lett. 302:213-216(1992).
-!- PTM: FIVE DISULFIDE BONDS ARE PRESENT (BY SIMILARITY).
-!- SIMILARITY: BELONGS TO THE CEREAL TRYPSIN/ALPHA-AMYLASE INHIBITOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Kirschner L.S., Horwitz S.B.;
Submitted (DEC-1991) to the EMBL/GenBank/DDBJ databases.
-I- FUNCTION: BNERGY-DEPENDENT BFFLUX PUMP RESPONSIBLE FOR DECREASED DRUG ACCUMULATION IN MULTIDRUG-RESISTANT (ELLS. MOUSE MDR2 IS NOT CAPABLE OF CONFERRING DRUG RESISTANCE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDLINE-88302195; PubMed=3405218;
Gros P., Raymond M., Bell J., Housman D.;
"Cloning and characterization of a second member of the mouse mdr
gene family.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         37; Indels 59;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CHAIN 28 162 SEED ALLERGENIC PROTEIN RAI7. SEQUENCE 162 AA; 17497 MW; EASCDE021FBA9348 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              01-MAY-1991 (Rel. 18, Created)
01-MAY-1991 (Rel. 18, Last sequence update)
11-MAY-1992 (Rel. 41, Last annotation update)
Mulliday resistance protein 2 (P-glycoprotein 2).
ABCB4 OR PGY2 OR PGY-2 OR MDR2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      InterPro; PR003612; AAI.
InterPro; IPR00168; Try/amyl inhbtr.
InterPro; IPR00108; Try/amyl inhbtr.
Pfam; Pr00234; tryp alpha amyl; 1.
PRINTS; PR00808; AMLASEINHBTR.
SNART; SM00499; AAI; 1.
PROSITE; PS00426; CEREAL TRYP AMYL INH; 1.
Allergen; Multigene family; Signal.
SIGNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRT; 1276 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        12.1%; Score 66.5; DE 21.5%; Pred. No. 3.5; tive 17; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Cell. Biol. 8:2770-2778(1988).
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                                                                                                                                                                                                                                                                                                                                                                                                                             EMBL; X66257; CAA46983.1; -. EMBL; D11431; BAA01997.1; -.
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HSSP; P01085; 1HSS.
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P21440;
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its way non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
-!- SUBCELLULAR LOCATION: Integral membrane protein.
-!- MISCELLANEOUS: IN MOUSE THE MDR GENE FAMILY INCLUDES THREE OR MORE
RELATED BUT DISTINCT CELLULAR GENES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          333 VFFSILIGAFSVGQAAPCIDAFANARGAAYVIFDIIDNNPKIDSFSERGHKPDNIKGNLE 392
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      28; Gaps
                                                                                    -!- SIMILARITY: BELONGS TO THE ABC TRANSPORTER FAMILY. MDR SUBFAMILY.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PROSITE; PS00211; ABC_TRANSPORTER; 2.
ATP-binding; Glycoprotein; Transmembrane; Transport; Repeat;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        12.0%; Score 66; DB 1; Length 1276; 20.4%; Pred. No. 25;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                19; Mismatches 31; Indels
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0827M3;
15-JUN-2002 (Rel. 41, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
- TIN-2002 (Rel. 41, Last annotation update)
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MGD; MGI:97569; Abcb4.
InterPro; IPR003593; AAA_ATPASe.
InterPro; IPR003439; ABC_transportr.
InterPro; IPR001140; ABC_transportr.
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CSGB OR STY1180.
Salmonella typhi.
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Pfam; PF00664; ABC membrane; 2.
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EMBL; M74151; AAA39515.1; -.
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PIR; A30409; DVMS2
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Best Local
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Parkhill J., Dougan G., James K.D., Thomson N.R., Pickard D., Wain J., Churcher C., Mungall K.L., Bentley S.D., Holden M.T.G., Sebaihia M., Baker S., Basham D., Brooks K., Chillingworth T., Connerton P., Cronin A., Davis P., Davies R.M., Dowd L., White N., Farrar J., Feltwell T., Hamlin N., Haque A., Hien T.T., Holroyd S., Jagels K., Krogh A., Larsen T.S., Leather S., Moule S., O'Gaora P., Parry C., Quail M., Rutherford K., Simmonds M., Skelton J., Stevens K., Whitehead S., Barrell B.G.;
"Complete genome sequence of a multiple drug resistant Salmonella enterica serovar Typhi CT18.";
                                                                                                                                                                                                                                                                                                                      OSL3 ARATH STANDARD; PRT; 244 AA. P50700; Q9T0D2; O1-OCT-1996 (Rel. 34, Created) 15-JUN-2002 (Rel. 41, Last sequence update) 15-JUN-2002 (Rel. 41, Last annotation update) Osmotin-like protein OSM34 precursor. OSM34 OR AT4G11650 OR T5C33.80.
Arabidopsis thaliana (Mouse-ear cress).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Nature 413:848-852(2001)

-I- FUNCTION: CURLIN IS THE STRUCTURAL SUBUNIT OF THE CURLI. CURLI AI

-ICOILED SURFACE STRUCTURES THAT ASSEMBLE PREFERENTIALLY AT GROWTH

TEMPERATURES BELOW 37 DEGREES CELSIUS. CURLI CAN BIND TO

FIBRONECTIN. THE MINOR SUBUNIT IS THE NUCLEATION COMPONENT OF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          the European Bioinformatics Institute. There are no restrictions use by non-profit institutions as long as its content is in modified and this statement is not removed. Usage by and for commodified and this statement is not removed.
                                                                                                      Capelli N., Diogon T., Greppin H., Simon P.; "Isolation and characterization of a cDNA clone encoding osmotin-like protein from Arabidopsis thaliana.";
                                                                                                                                                                                                                                                                      Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosiceurosids II; Brassicales; Brassicaceae; Arabidopsis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation -
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    STRAIN=cv. Columbia;
MEDLINE=20083488; PubMed=10617198;
                                                                                    osmotin-like protein
Gene 191:51-56(1997).
                                                                                                                                                                                        SEQUENCE FROM N.A.
STRAIN=cv. Columbia; TISSUE=Leaf;
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                                           SEQUENCE FROM N.A
                                                                                                                                                                       MEDLINE=97354294; PubMed=9210588;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   s requires a license agreement (See http://www.isb-sib.ch/announce/an email to license@isb-sib.ch).
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31.0%;
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Pred. No. 4.2;
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RA Vos P., Hohetseld J., Zimmermann W., Wedler H., Ridley P.,
RA Langham S.-A., McCullagh B., Bilham L., Robbern J.,
RA Van der Schweren J., Grymonprez B., Chuang X.-J., Vandenbussche F.,
RA Van der Schweren J., Grymonprez B., Chuang X.-J., Vandenbussche F.,
RA Wan der Schweren J., Woet M., Bastiaens I., Aert R., Defoor E.,
RA Holzer E., Brandt A., Peters S., Van Staveren M., Dirkee W.,
RA Holzer E., Brandt A., Peters S., Van Staveren M., Dirkee W.,
RA Mooijman P., Klein Lankhorst R., Rose M., Hamberth S., Van den Daele H.,
RA De Keyser A., Buysshaert C., Gielen J., Villarroel R., De Clercq R.,
RA Clark L., Dogett J., Hall S., Kay M., Lennard N., McLay K., Mayes R.,
RA Clark L., Rajandream M.A., Lyne M., Benes V., Rechmann S.,
RA Clark L., Rajandream M.A., Lyne M., Benes V., Rechmann S.,
RA Clark L., Rajandream M.A., Lyne M., Benes V., Rechmann S.,
RA Clark J., Willer R., Scharfe M., Grimm M., Loehnert T.-H.,
RA Borkova D., Bloecker H., Scharfe M., Grimm M., Loehnert T.-H.,
RA Massenet O., Quigley F., Clabauld G., Muendlein A., Felber R.,
RA Massenet O., Quigley F., Clabauld G., Muendlein A., Felber R.,
RA Chefdor F., Cooke R., Berger C., Monfort A., Casacuberta E.,
RA Chefdor F., Cooke R., Benger C., Monfort A., Casacuberta E.,
RA Reinen L., Schwarz S., Scholler P., Hobers S., Tacon D., Jesse T.,
RA Reinen L., Schwarz S., Scholler P., Hober S., Francs P., Bielke C.,
RA Parnell L., Dedha N., Wilson R.K., de la Bastide N., Habermann K.,
RA Schonh M., Marray J., Sheet P., Cordes M., Abort R., Schotz K., Johnson D.,
RA Schonh M., Marray J., Sheet P., Cordes M., Abort R., Schot K., Johnson D.,
RA Minx P., Bentley D., Fulton B., Miller N., Greco T., Kemp K.,
RA Melson J., Spieth J., Ryan E., Andrews S., Geisel C., Layman D.,
RA Melson J., Spieth J., Ryan E., Andrews S., Geisel C., Layman D.,
RA Melson J., Stond S., Johnson R.K., Haller A., Johnson A.,
RA Melson J., Schauf K., Merker M., Watero A., Shah R.,
RA Schonh M., Martay J., Sheet P., Cordes M., Martay A., Moordan C.,
RA Martin J., Schotz K., Merker M., Melson
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    Puigdomenech P., Watson
  POTENTIAL.
OSMOTIN-LIKE PROTEIN OSM34.
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Saccharomyces cerevisiae.";
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P04806;
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Adachi T., Izumi H., Yamada T., Tanaka K., Takeuchi S.,
Nakamura R., Matsuda T.;
Gene structure and expression of rice seed allergenic proteins
belonging to the alpha-amylase/trypsin inhibitor family.";
Plant Mol. Biol. 21:139-248(1993).
-i- PTM: FIVE DISULFIDE BONDS ARE PRESENT (BY SIMILARITY).
                                                                                                                                                                                                                                                                              Gaps
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Spermatophyta, Magnoliophyta, Liliopsida, Poales, Poaceae,
Ehrhartoideae, Oryzeae, Oryza.
                                                                                                                                                                                                                                                                                 17;
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E -> V (IN REF. 1).
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01-JUN-1994 (Rel. 29, Last sequence update)
01-JUN-1994 (Rel. 29, Last annotation update)
                                                                                                                                                                                                                                                    Pred. No. 6.5;
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InterPro; IPR003612; AAI.
InterPro; IPR001768; Try/amyl_inhbtr.
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PRINTS; PR00808; AMLASEINHBTR.
SMART; SM00499; AAI; 1.
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Gaps

72;

Conservative

31;

Marches

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61 ROCVGTRSPGAVDEQLAQDCCRELAAVDDSWCRCSALNHMVGG------IYRELG 109
   -----GSAFTVWSGPGCNNRAE 42
                     Eki T., Naitou M., Hagiwara H., Ozawa M., Sasanuma S.-I., Sasanuma W., Tsuchiya Y., Shibata T., Hanacka F., Murakami Y.; Asasanuma M., Tsuchiya S. DNA sequence including the right telomere of chromosome VI from Saccharomyces cerevisiae.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          X-RAY CRYSTALLOCRAPHY (3.5 ANGSTROMS).
MEDLINE-81049624; Pubmed=7001031;
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"Structure of a complex between yeast hexokinase A and glucose. I.
Structure determination and refinement at 3.5-A resolution.";
                                                                          -----SKCGCSAI-HQKGGYDFSYTGQTAALYNQAG
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                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota, Fungi, Ascomycota, Saccharomycotina, Saccharomycetes,
Saccharomycetales, Saccharomycetaceae, Saccharomyces
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Stachelek C., Stachelek J., Swan J., Botstein D., Konigsberg W., "Identification, cloning and sequence determination of the genes specifying hexokinase A and B from yeast.";
Nucleic Acids Res. 14:945-963(1986).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDLINE-88227998; PubMed-3131329;
Tamura J.K., Ladime J.R., Cross R.L.;
"The adenine nucleotide binding site on yeast hexokinase PII.
Affinity labeling of Lys-11 by pyridoxal
5'-diphospho-5'-adenosine.";
J. Biol. Chem. 263:7907-7912(1988).
                                                                                                                                                                                                                                                                                                                     13-AUG-1987 (Rel. 05, Created)
01-NOV-1995 (Rel. 32, Last sequence update)
15-UUN-2002 (Rel. 41, Last annotation update)
15-UUN ECC 2.7.1.1) (Hexokinase PI).
HXK1 OR HKA OR YPR053C.
                                                                                                                                                                                                                                                                                       485 AA
MASTKLFFS--VITVMMLIAMASEMVN-----
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MEDLINE=95400292; PubMed=7670463;
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MEDLINE=86083199; PubMed=3908224;
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STRAIN=S288c / AB972;
MEDLINE=96287652; PubMed=8686379;
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Gene 39:95-102(1985).
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EMBL; M14410; AAA34698.1; -.
EMBL; X03402; CAA27202.1; -.
EMBL; D50617; BAA09292.1; -.
PIR; A24531; KIBYHA.
PIR; A24531; KIBYHA.
PIR; A28178; A28178.
PDB; 14KG; 15-OCT-91.
SWISS-2DPAGE; P04806; YEAST.
SWISS-2DPAGE; P04806; YEAST.
SGD; S0001949; HXK1.
InterPro; IPR001312; Hexokinase.
Pfam; PF00349; hexokinase; 1.
Pfam; PF00349; hexokinase; 1.
Pfam; PF003727; hexokinase; 1.
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                                                                                                                                                                                                                                                                                                                               DOMAIN
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SUBUNIT: HOMODIMER.
MISCELLANEOUS: IN YEAST THERE ARE THREE GLUCOSE-PHOSPHORYLATING
ISOENZYMES, DESIGNATED HEXOKINASE I, II AND GLUCOKINASE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ISOENZYMES, DESIGNATED HEXOKINASE I, II AND G SIMILARITY: BELONGS TO THE HEXOKINASE FAMILY. DATABASE: NAME=Worthington enzyme manual;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WWW="http://www.worthington-biochem.com/manual/H/HK.html".
                                                                                                    19
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91
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ATP.

GLUCOSE-BINDING (POTENGE)

G-V (IN REF. 1).

H-> R (IN REF. 1).

V-> C (IN REF. 1).

EN -> VF (IN REF. 1).

I-> M (IN REF. 1).

I-> M (IN REF. 2).

J-> EN (IN REF. 2).

SL -> VS (IN REF. 1).
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                   Matches
                     Query Match
Best Local :
                               SEQUENCE
440
         391
             40 RAERYSKCGCSAIHOKGGYDFSYTGQTAALYN-----QAGCSGVAHTRFGSSARACNPF 93
    94
    Q.
         RAARLAVCGIAAICOKRGYKTGHIAADGSVYNKYPGFKEAAAKGLR------DIY 439
GW 441
                  ll Similarity 27.4
    95
                            AA;
                                 53738 MW;
                     11.7%;
                   Score 64.5; DI
Pred. No. 15;
9; Mismatches
                   9
                             AF5C9DA8F17BC3D0 CRC64;
                        DB 1; Length
                   19;
                   Indels 17;
                        485;
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Search completed: January 12, 2003, 09:36:39 Job time : 27 secs

Gaps

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Title:
Perfect score:
Sequence:
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Maximum Match 100%
Listing first 45 summaries
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Maximum DB seq length: 200000000
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1: sp_archea:*
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3: sp_fungi:*
4: sp_human:*
5: sp_invertebrate
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551
1 MASTKLFFSVITVMMLIAMA......FGSSARACNPFGWKSIFIQC 102
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                                                                                                                                                                                                                                                                                                                                                                                                         671580 seqs, 206047115 residues
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                                                                                                                                                                                                                                                                                                                                                                                                                                      Gapop 10.0 , Gapext 0.5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GenCore version 5.1.3
Copyright (c) 1993 - 2003 Compugen Ltd.
                                                                                                                  sp_mhc:*
sp_organelle:*
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sp_archeap:*
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sp_mammal:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

12.5 668 6 Q8WNU6 Q8wnu6	12.3 184 5 0 12.2 307 12 12.2 653 12 12.2 1486 4 0 12.2 2121 12	Result S	Score -77.5 75.5 75.5 79.5 70 70 69.5 69.5	Query Query 114.1 113.7 113.7 112.5 5 112.5 5 112.5 5	Length DB 1486 3 1558 5 254 5 730 2 307 1 307 1 532 1 1532 1 1780 6	DB 55 122 122 122 122 123 133 133 133 133 133	SUMMARIES ID 005838 Q9BLR5 Q9BLR5 Q9667 Q9WQ79 Q9WQ80 Q8YD38 Q8YD38 Q8YD38 Q8YD38 Q8WUG	Description Q05838 saccharomyc Q9blr5 leishmania Q45025 hydra magni Q07667 enterococcu Q9wq79 feline infe Q9wq80 canine coro Q8yd38 brucella me Q57484 gallus gall Q8wnu6 canis famil
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11.6	1 - 0	1	11.5	11.6	11.6	11.6	11.7	11.7	11.8	11.8	11.8	11.8	11.9	11.9	11.9			:-			12.0	12.0	12.0	12.1	12.1	12.1	12.1	12.1	12.2
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Q8ymu3 anabaena sp	Q92416 rattus norv		٠,		J	Q9bkb4 mesobuthus	3 gall			Q8w3y6 persea amer	\circ	Q94476 dictyosteli	_	aenorhabdi	(J)			Q9tsu2 felis silve	074996 yarrowia li		œ	caenorhabd			-	3			Q9iw06 transmissib

ALIGNMENTS

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8 FSVITVNMLIAMASEMVNGSAFTVWSGPGCNNRAERYSKCGCSAIHQKGGYDFSYTG 64 	Query Match 14.1%; Score 77.5; DB 3; Length 486; Best Local Similarity 31.2%; Pred. No. 2; Matches 30; Conservative 8; Mismatches 27; Indels 31; Gaps	Q05838 PRELIMINARY; PRT; 486 AA. Q05838; Q1-NOV-1996 (TrEMBLrel. 01, Created) Q1-NOV-1996 (TrEMBLrel. 21, Last sequence update) Q1-JUN-2002 (TrEMBLrel. 21, Last annotation update) Hexokinase PI (HXK2). HXZ OR YGL25W. Saccharomyces cerevisiae (Baker's yeast). Eukaryota; Fungi; Ascomycota; Saccharomycetales; Saccharomycetales; Saccharomycetaceae; Saccharomycees. NCBI_TaxID=4932; [1] SEQUENCE FROM N.A. MEDLINE=86083199; PubMed=3908224; KOpetzki E., Entian K.D., Mecke D.; "Complete nucleotide sequence of the hexokinase PI gene (HXK1) of Saccharomyces cerevisiae."; Gene 39:95-101(1985). EMBL; M1441; AAA34699.1; HSSP; P13367; 1QHA. SGD; S0003222; HXK2. INterPro; IFR001312; Hexokinase. Pfam; PF00349; hexokinase; 1. Pfam; PF00379; hexokinase; 1. PRINTS; PR00475; HEXOKINASE. PRODOM; PD001109; Hexokinase; 1. SEQUENCE 486 AA; 53952 MW; 218F5AC9B8C36C8C CRC64;	JUT 1

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RESULT 5
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           711 LHNSDPWRGVVDAAVRCYTDDAGCSGQAHEGPALGSLGRCLLLAIWLSLALVDVDGGVGA 770
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              10 VITVMMLIAMASEMVNGSAFTVWSGPGCNNRAERY-SKCGCSAIHQKGGYDFSYTGQTAA 68
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Eukaryota; Euglenozoa; Kinetoplastida; Trypanosomatidae; Leishmania.
VCBI_TaxID=5664;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Tosato V., Ciarloni L., Bianchettin G., Bruschi C.V., Ivens A.C., Quail M., Rajandream M.A., Barrell B.G.; submitted (FEB-2001) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Hydra magnipapillata (Hydra).
Eukaryota, Metazoa, Cnidaria, Hydrozoa, Hydroida, Anthomedusae,
Hydridae, Hydra.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity 24.6%; Pred. No. 11;
Matches 32; Conservative 10; Mismatches 33; Indels 55
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STRAIN=FRIEDLIN;
MEDLINE=98146435; PubMed=9477341;
Ivens A.C., Lewis S.M., Bagherzadeh A., Zhang L., Chan H.M., Smith D.F.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           "A physical map of the Leishmania major Friedlin genome."; Genome Res. 8:135-145(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1558 AA; 165803 MW; BB029575FDED8265 CRC64;
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01-JUN-1998 (TrEMBLrel. 06, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                            01-JUN-2001 (TrEMBLrel. 17, Last sequence update) 01-DEC-2001 (TrEMBLrel. 19, Last annotation update) Hypothetical 165.8 kDa protein.
                                                                          413 HIAA-----DGSVSTRYPGFKEKAANALKDIYGW 441
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Interpro; IPR001865; Ribosomal S2.
PROSITE; PS00962; RIBOSOMAL_S2_1; UNKNOWN_1.
SPOCHAETAL PACEAL S2.
SEQUENCE 1558 AA; 165803 MW; BB029575FDEI
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                                                                                                                                                                                                                                                              PRT; 1558 AA
       65 QTAALYNQAGCSGVAHTRF-GSSARACNP----FGW
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                                                                                                                                                                                                                                                                      PRELIMINARY;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Leishmania major.
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"The division and cell wall gene cluster of Enterococcus hirae S185.";

"The division and cell wall gene cluster of Enterococcus hirae S185.";

"The division and cell wall gene cluster of Enterococcus hirae S185.";

"Therefore IPR04225; PBP Cterm.

InterPro; IPR004225; PBP Cterm.

InterPro; IPR00451; PBP Gimer.

InterPro; IPR00460; Transpeptidae.

Pfam; PF03717; PBP Gimer; 1.

Pfam; PF03717; PBP Gimer; 1.

Pfam; PF030905; Transpeptidase; 1.

SEQUENCE 730 AA; 80947 MW; C928FFICI0E810BB CRC64;
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Viruses; ssRNA positive-strand viruses, no DNA stage; Nidovirales;
Coronaviridae; Coronavirus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Bacteria, Firmicutes, Bacillus/Clostridium group, Lactobacillales,
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B)
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                                                                                                     / Match 13.6%; Score 75; DB 5; Length 254; Local Similarity 27.3%; Pred. No. 1.9; les 24; Conservative 14; Mismatches 24; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              26 GSAFTVWSGPGCNNRAERYSKCGCSAI-HQKGGYDFSYTGQTAALYN 71
J. Cell Sci. 111:1545-1554(1998),
EMBL; AF043907; AAC39121.1; -.
SEQUENCE 254 AA; 25393 MW; 649BAB00B3BEABF9 CRC64;
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Last annotation update)
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MEDLINE=99319897; PubMed=10392726;
Stephensen C.B., Casebolt D.B., Gangopadhyay N.N.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-JAN-1998 (TrEMBLrel. 05, Last sequence update) 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              730 AA.
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01-NOV-1999 (TrEMBLrel. 12, Last seq
01-NOV-1999 (TrEMBLrel. 12, Last ann
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                                                                                                                                                                                                                                                                                                                                                                       49 AGCCNGLAHGGHHGGAYGQAAHHAGGYG 76
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                                                                                                                                                                                                                                                                                                                      73 AG-CSGVAH-----TRFGSSARACNPFG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Enterococcaceae; Enterococcus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRELIMINARY;
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Best Local Similarity
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                                                                                                                Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            007667;
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RESULT 6
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AC Q8
AC Q8
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Best Local Similarity
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Virus Res. 60:181-189(1999).
EMBL; AF124987; AAD32991.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-NOV-1999 (TrEMBLrel. 12,
01-NOV-1999 (TrEMBLrel. 12,
01-NOV-1999 (TrEMBLrel. 12,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Q9WQ80
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              "Phylogenetic analyais of a highly conserved region of the polymerase gene from 11 coronaviruses and development of a consensus polymerase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NON TER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Chain reaction assay.";
Virus Res. 60:181-189(1999).
EMBL; AF124986; AAD32990.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Stephensen C.B., Casebolt D.B., Gangopadhyay N.N.; "Phylogenetic analysis of a highly conserved region of the polymerase gene from 11 coronaviruses and development of a consensus polymerase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Viruses; ssRNA positive-strand viruses, no DNA stage; Nidovirales; Coronaviridae; Coronavirus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RNA-directed RNA polymerase
                            01-MAR-2002 (TrEMBLrel. 20, Created)
01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
Alcohol dehydrogenase (Acceptor) (EC 1.1.99.-).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RNA-directed RNA polymerase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDLINE=99319897; PubMed=10392726;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NCBI_TaxID=11153;
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     BMEII0339
                                                                                                                                    Q8YD38;
                                                                                                                                                                    Q8YD38
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                                                                                                                                                                                                                                                                                                         179
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  69 LYNQAGCSGVAHTRF------GSSARACNPFGWKSI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             16 LIAMASEMVNGSAFTVWSGPGCNNRAERYSKCG-----CSAIHOKGGYDFSYTGQTAA 68
                                                                                                                                                                                                                                                                                                                                                              69
                                                                                                                                                                                                                                                                                                                                                                                                                                                               16 LIAMASEMVNGSAFTVWSGPGCNNRAERYSKCG-----CSAIHQKGGYDFSYTGQTAA 68
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Local
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                                                                                                                                                                                                                                                                                                      ----DGTTAYANSAFNIFQAVSANVNKLLGVDSNACNNVTVKSI 218
                                                                                                                                                                                                                                                                                                                                                         LYNQAGCSGVAHTRF------GSSARACNPFGWKSI 98
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307 AA;
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307 AA;
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ilarity 25.0%; Pred. No. 8
Conservative 13; Mismatche
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Pred. No. 8.
                                                                                                                                                                      PRT;
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RESULT 8
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Best Local :
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             HSSP; P02468; IKLO.
InterPro; IPR002106; AAtRNA ligaseII.
InterPro; IPR002516; EGF-like.
InterPro; IPR002049; Laminin EGF.
InterPro; IPR001886; LamNT.
Pfam; PF00053; laminin EGF; 13.
Pfam; PF00053; laminin Neerm; 1.
PRINTS; PR00011; EGFLAMININ.
SMART; SM00180; EGF Lam; 13.
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MEDLINE=20020109; PubMed=11756688;
DelVecchio V.G., Kapatral V., Redkar R.J., Patra G., Mujer C., Los
Ivanova N., Anderson I., Bhattacharyya A., Lykidis A., Reznik G.,
Jablonski L., Larsen N., D'Souza M., Bernal A., Mazur M., Goltsman
Selkov E., Elzer P.H., Hagius S., O'Callaghan D., Letesson J.-J.,
Haselkorn R., Kyrpides N., Overbeek R.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              "The genome sequence of the facultative intracellular pathogen Brucella melitensis.";
Proc. Natl. Acad. Sci. U.S.A. 99:443-448(2002).
EMBL; AE009671; AAL53581.1; -.
Interpro; IPR000172; GMC_oxred.
Pfam; PF00732; GMC_oxred.
Pfam; PF00732; GMC_oxred; 1.
Oxidoreductase; Complete proceome.
Oxidoreductase; Complete proceome.
SEQUENCE 532 AA; 58225 MW; F15857645D149ADD CRC64;
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057484;
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Brucellaceae; Brucella.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-JUN-1998 (TrEMBLrel. 06, Created)
01-JUN-1998 (TrEMBLrel. 06, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
101-JUN-2002 (TrEMBLrel. 21, Last annotation update)
101-JUN-2002 (TrEMBLrel. 21, Last annotation update)
101-JUN-2002 (TrEMBLrel. 21, Last annotation update)
101-JUN-1998 (TrEMBLrel. 06, Created)
101-JUN-1998 (TrEMBLrel. 06, Last sequence update)
101-JUN-2002 (TrEMBLrel. 21, Last sequence update)
101-JUN-2002 (TrEMBLrel. 21,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A. MEDLINE=93015947; PubMed=1400373;
                                                                                                                                                                                                                                                                       "Primary structure and expression of a chicken laminin beta chain: evidence for four beta chains in birds.";
Matrix Biol. 16:471-481(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             O'Rear J.J.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NCBI
                                                                                                                                                                                                                                                  EMBL; AF038555; AAB92586.1;
                                                                                                                                                                                                                                                                                                                                                                              MEDLINE=98209634; PubMed=9550264;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                "A novel
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                                                                                                                                                                                                                                                                                                                                                       Liu J.,
                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                        Biol.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TaxID=9031;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   -----WGWDDV 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FTTEAEPGLNGRSLNYPRGKVLGGCSSINGMIYMRGQACDYD-----LWRQAGCDG 114
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 22;
SM00180;
SM00136;
                                                                                                                                                                                                                                                                                                                                                       Swasdison S., Xie W., Brewton R.G.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                           Chem.
                                                                                                                                                                                                                                                                                                                                                                                                                                                        laminin Bl chain variant in Chem. 267:20555-20557(1992)
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  EGF_Lam; 13
LamNT; 1.
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Pred. No. 17
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   avian
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     eye.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    16;
                                                                                                                                                                                                                                                                                                                                                            Mayne
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Indels
                                                                                                                                                                                                                                                                                                                                                               20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mujer C., Los T., Reznik G.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Phasianinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         35;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          77
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                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                      ----SKCGCSAIHQKGGYD 59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 6 LFFSVITVMMLIAMASEMV-----NGSAFTVWSGPGCNNRAERYSKCGCSAIHQKGGYD 59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Canis familiaris (Dog).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Carnivora, Fissipedia, Canidae, Canis.
PROSITE; PS00339; AA TRNA_LIGASE II_2; UNKNOWN_1.
PROSITE; PS01022; EGF_1; UNKNOWN_10_
PROSITE; PS01186; EGF_2, 2.
PROSITE; PS01248; LAMININ TYPE EGF; 12.
EGF-like domain; Glycoprotein; Laminin EGF-like domain; Repeat.
SEQUENCE 1792 AA; 195723 MW; 4A4CBE0206F6A600 CRC64;
                                                                                                                                                                                                                                                                                                                    25;
                                                                                                                                                                                                                                              Query Match 12.6%; Score 69.5; DB 13; Length 1792; Best Local Similarity 25.0%; Pred. No. 61; Matches 25; Conservative 9; Mismatches 41; Indels 25;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.

A Uozumi K., Nakaichi M.;

"Canine MDL";

"Canine MDL";

"Submitted (JUL-2001) to the EMBL/GenBank/DDBJ databases.

EMBL; AB066299; BAB83959.1;

"InterPro; IPR0013593; AAA_ATPase.

R InterPro; IPR001409; ABC_transportr.

R Ffam; PP000664; ABC_membrane; 2.

R Pfam; PP0000654; ABC_transportr; 1.

R Pfam; PP0000065; ABC_transportr; 1.

R ProDom; PD0000066; ABC_transportr; 1.

R SMART; SM00382; AAA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            668 668
668 AA; 73546 MW; FBCD80F7C934B31A CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            01-MAR-2002 (TrEMBLrel. 20, Created)
01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
Multidrug resistance p-glycoprotein (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-JUN-1998 (TrEMBLrel. 06, Created)
01-JUN-1998 (TrEMBLrel. 06, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
Multidrug resistance p-glycoprotein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         360 MAVFLATGNTSG----AVCDGCQHNTMGRHCHLCKPFYYK 395
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             60 ---FSYTGQTAALYNQAGCSGVAHTRFGSSARACNPFGWK 96
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    145 FKNVHFSYPSRKEVKILKGLNLKVQSGQTVALVGNSGC 182
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        75
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PROSITE, PS00211; ABC_TRANSPORTER; UNKNOWN_1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRT; 1280 AA.
                                                                                                                                                                                                                                                                                                                                                                                   18 AMASEMVNGSAFTVWSGPGCN-NRAERY------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ----FSY-----TGQTAALYNQAGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NCBI_TaxID=9615;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Local Sim.
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SEQUENCE
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046605
AD 046605
DT 01-JUN
DT 01-JUN
DT 01-JUN
DT 01-JUN
DT MULTIC
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Schwarz-Romond T., Asbrand C., Bakkers J., Kuhl M., Schaeffer H.-J., Huelsken J., Behrens J., Hammerschmidt M., Birchmeier W.; "The Ankyrin Repeat Protein Diversin Acts in the Wnt Signaling Pathway and Controls Embryonic Axis Formation."; Submitted (JAN-2001) to the EMBL/GenBank/DDBJ databases.

EMBL, AY026320; AAK1S806.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    :||||:
335 VFFSVLIGAFSIGQASPSIEAFANARGAAYEIFKIIDNKPSIDSYSKSGHKPDNIKGNLE 394
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     28; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             6 LFFSVITVMMLIAMASEMV-----NGSAFTVWSGPGCNNRAERYSKCGCSAIHQKGGYD 59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    20; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 MASTKLFFSVITVMM-------LIAMASEMVNGSAFTVWSGPGCNNRAERYS 45
Canis familiaris (Dog).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Carnivora, Fissipedia, Canidae, Canis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mus musculus (Mouse).
Eukaryota, Metazoa; Chordata, Craniata, Vertebrata, Euteleostomi;
Mammalia; Eutheria; Rodentia, Sciurognathi; Muridae; Murinae; Mus.
                                                                                                                                                                              EMBL, APC45016, AAC22113.1, -...

InterPro; IPR001369; AAA ATPase.
InterPro; IPR001349; ABC Transportr.

R InterPro; IPR001349; ABC transportr.

R Pfan; PF00664; ABC membrane; 2.

R ProDom; PD000005, ABC transportr; 2.

R SWART; SM00302; AAA; 2.

R PROSITE; PS00211; ABC TRANSPORTER; 2.

R PROSITE; PS00211; ABC, TANSPORTER; 2.

R ATP-binding; Transport.

SEQUENCE 1280 AA; 141524 MW; 762DD5AFF4C73306 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 12.5%; Score 69; DB 6; Length 1280; Best Local Similarity 25.5%; Pred. No. 48; Matches 25; Conservative 12; Mismatches 33; Indels ;
                                                                                                                             Puel O., Lepage J.F., Alvinerie M., Galtier P., Pineau T.,
Submitted (JAN-1998) to the EMBL/GenBank/DDBJ databases.
-!- SIMILARITY: BELONGS TO THE ABC TRANSPORTER FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          12.3%; Score 68; DB 11; Length 712; 23.5%; Pred. No. 34; tive 21; Mismatches 37; Indele ::
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PROSITE; PS50088; ANK REPEAT; 6.
PROSITE; PS50297; ANK REP REGION; 1.
SEQUENCE 712 AA; 77934 MW; BC0344DA544E731A CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       395 FKNVHFSYPSRKEVKILKGLNLKVQSGQTVALVGNSGC 432
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     60 ----FSY------TGQTAALYNQAGC 75
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-WAR-2002 (TrEMBLrel. 20, Created)
01-WAR-2002 (TrEMBLrel. 20, Last seq
01-JUN-2002 (TrEMBLrel. 21, Last anno
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              InterPro; IPR002110; ANK.
Pfam; PF00023; ank; 8.
PRINTS; PR01415; ANKYRIN.
SMART; SM00248; ANK; 8.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Matches 24; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRELIMINARY;
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                                                                                           SEQUENCE FROM N.A.
                                                        NCBI_TaxID=9615;
                                                                                                                TISSUE=COLON;
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Best Local !
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Bonfield J., Burton J., Connell M., Copsey T., Cooper J., Coulson A.,
Craxton M., Dear S., Du Z., Durbin R., Favello A., Fulton L.,
Gardner A., Green P., Hawkins T., Hillier L., Jier M., Johnston L.,
Jones M., Kershaw J., Kirsten J., Laister N., Latreille P.,
Lightning J., Lloyd C., McMurray A., Mortimore B., O'Callaghan M.,
Parsons J., Percy C., Rifken L., Roopra A., Saunders D., Shownkeen R.
Smaldon N., Smith A., Sonnhammer E., Staden R., Sulston J.,
Thierry-Mieg J., Thomas K., Vaudin M., Vaughan K., Waterston R.,
Wateson A., Weinstock L., Wilkinson-Sproat J., Wohldman P.,
"2.2 Mb of contiguous nucleotide sequence from chromosome III of C.
         Viruses; ssRNA
                                                                    01-NOV-1999
01-DEC-2001
                                                                                                                                                                                                                                                                                                                                                                                         Waterston R.; Submitted (JIN-1995) to the EMBL/GenBank/DDBJ databases. EMBL; U28731; AAA68294.1; -. PRIONONEMOCEDITES PROCES
                                                                                                                                                                                                                                                                                                                                                                                                                                                   STRAIN=BRISTOL N2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STRAIN-BRISTOL N2;
                                                                                                                                                                                               138 -----GYSGYG-----GGYPGMYGGGMGGSYGSSSWGSYSSSRSG 172
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Submitted (JUN-1995) to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Geisel C.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Nature 368:32-38(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
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Q09943;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDLINE=94150718; PubMed=7906398;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STRAIN=BRISTOL N2;
                 ransmissible gastroenteritis virus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NCBI_TaxID=6239;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Rhabdītidae; Peloderinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Caenorhabditis elegans.
Eukaryota; Metazoa, Nematoda, Chromadorea, Rhabditida, Rhabditoidea,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      01-NOV-1996 (TrEMBLrel. 01, Created)
01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            F12A10.1 protein.
                                                                                                                                                                                                                              37 CNNRAERYSKCGCSAIHQKGGYDFSYTGQTAALYNQAGCSGVAHTRFG 84
                                                                                                                                                                                                                                                                    78
                                                                                                                                                                                                                                                                                                                                              Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            106 KDGNTALHEAAWHGFS---QSAKLLVKAGANVLARNKAGNTA 144
                                                                                                                                                                                                                                                                                       QUENCE FROM N.A.
                                                                                                                                                                                                                                                         MHSTTLFFVVFGILVAVSLAFDDLNHPKNLQWRSSEGSRVKRWGGWGGGYPGGYGGGYPG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 sequence of C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         KCGCSAIHQKGGYDFSYTGQTAALYNQAGCSGVAHTRFGSSA
                                                                                                                                                                                                                                                                                                                                              Similarity
                                              (TrEMBLrel. 12, Created)
(TrEMBLrel. 12, Last sequence
(TrEMBLrel. 19, Last annotate
d RNA polymerase (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                       184 AA;
                                                                                                                           PRELIMINARY;
                                                                                                                                                                                                                                                                                                                              Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRELIMINARY;
    positive-strand viruses,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               elegansto the
                                                                                                                                                                                                                                                                                                                                                                                   20062 MW; EF19A9A6C96B175A CRC64;
                                                                                                                                                                                                                                                                                                                                         12.3%;
                                                                                                                                                                                                                                                                                                                       11; Mismatches 34; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Caenorhabditis
                                                            Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           cosmid F12A10.";
EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                       Score 67.5;
Pred. No. 9.
                                                                                                                           PRT;
                                                                                                                         307 AA.
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DNA stage; Nidovirales;
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RESULT 14
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                                                     IJkel W.F.J., van Strien E.A., Heldens J.G.M., Broer R., Goldbach R.W., Vlak J.M.;
Submitted (JUL-1999) to the EMBL/GenBank/DDBJ databases.
EMBL; AF169823; AAF33660.1; -.
SEQUENCE 653 AA; 74213 MW; DADAD68F070FE0BC CRC64;
                                                                                                                                                                                                                                                                                                                                                                      MEDLINE=93286555; PubMed=8509757;
Zuidema D., van Oers M.M., van Strien E.A., Caballero P.C., Klok E.J.,
Goldbach R.W., Vlak J.M.;
                                                                                                                                 SEQUENCE FROM N.A.
                                                                                                                                                                                                                                       Goldbach R.W., Vlak J.M.; "Sequence and organization of the spodoptera exigua multicapsid
                                                                                                                                                                                                                                                                           IJkel W.F.,
                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A. MEDLINE=20036646; PubMed=10567663;
                                                                                                                                                                                                                                                                                                                               Spodoptera exigua nuclear polyhedrosis virus. n. Gen. Virol. 74:1017-1024(1993).
                                                                                                                                                                                                                                                                                                                                                       "Nucleotide sequence and transcriptional analysis of the p10 gene
                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE OF 596-653 FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Spodoptera exigua nucleopolyhedrovirus.
Viruses, dsDNA viruses, no RNA stage, E
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01-OCT-2000
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EMBL; AF124992; AAD32996.1; -.
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Stephensen C.B., Casebolt D.B., Gangopadhyay N.N.,
"Phylogenetic analysis of a highly conserved regio
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE
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                    Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       69 LYNQAGCSGVAHTRF------GSSARACNPFGWKSI 98
                                                                                                                                                                                                                   Gen. Virol. 80:3289-3304(1999).
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                                                                                                                                                                                                                               eopolyhedrovirus genome."
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                    Similarity
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307 AA;
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12.2%; Score 67; DB 12; Length 653; 33.3%; Pred. No. 40; tive 9; Mismatches 15; Indels
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AN 113 A DATE OF SEQUENCE FROM N.A.

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AN EDLINE-98055454; PubMed=9195076;

AN EDLINE-98055454; PubMed=9195076;

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12.2%; Score 67; DB 4; Length 1486;
Best Local Similarity 28.1%; Pred. No. 95;
Matches 27; Conservative 8; Mismatches 23; Indels 38; Gaps
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                                                    Eukaryota, Merazoa; Chordata; Craniata; Vertebrata, Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
43 RYSKCGCSAI-----HQKGGYD-----FSYTGQTAALYNQAGC---SGVAHTRFGS 85
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Homo sapiens (Human).
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Search completed: January 12, 2003, 09:38:22 Job time : 84 secs

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Listing first 45 summaries
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SUMMARIES

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ALIGNMENTS

REFERENCE AUTHORS	SOURCE ORGANISM	ACCESSION VERSION KEYWORDS	LOCUS DEFINITION	RESULT 1 MIRNAAP1
Macadamia. 1 (bases 1 to 493) Marcus, J.P., Goulter, K.C., Green, J.L., Harrison, S.J. and Manners, J.M.	Macadamia integrifolia. Macadamia integrifolia Macadamia integrifolia Eukaryota, Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; Proteaceae;	Y10903.1 GI:2181942 AMP1 gene.	MIRNAAP1 493 bp mRNA linear PLN 05-JUN-1997 M.integrifolia mRNA for antimicrobial protein 1.	

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/translation="MASTKLPFSVITVMMLIAMASEMVNGSAFTVWSGPGCNNRAERY
skcGcSaihqkGgydFsytGQTAALYNQAGCSGVAHTRFGSSARACNPFGWK8IFIQC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ö
Purification, characterisation and cDNA cloning of an antimicrobial
                                                                                                                                       Submitted (30-JAN-1997) J.P. Marcus, Cooperative Research Centre for Trop., Plant pathology., 5th Level John Hines Building., The University of Queensland., Brisbane, QLD 4072, AUSTRALIA Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             240
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    241 hárgacrrcadcracacrddadcaaacrdcrdcrcrcraaaccaddragardcaagacrddardaard
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                                                                                                                                                                                                                                       organism="Macadamia integrifolia"
                                                                                                                                                                                                                                                                                                                                                                                  'Function="antimicrobial protein"
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99.9%; Score 492.6; DB 8;
Best Local Similarity 100.0%; Pred. No. 3.2e-121
Matches 493; Conservative 0; Mismatches 0;
                    peptide from Macadamia integrifolia
Eur. J. Biochem. 244 (3), 743-749 (1997)
97261828
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                                                                                                                                                                                                                                                                                                                                                                                                                    /proteIn_id="CAA71842.1"
/db_xref="G1:2181943"
                                                                                                                                                                                                                                                           /db_xref="taxon:60698"
/clone="pGM7*2"
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70. 378
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148. .375
/gene="AMP1"
                                                                                                                                                                                                                                                                                                                               gene="AMP1"
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                                                                                               2 (bases 1 to 493)
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                                                                                                                                 Direct Submission
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                                                                                                                Marcus, J. P.
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Direct Submission

Direct Submission

Submitted (121-MAR-2001) Sanger Centre, Hinxton, Cambridgeshire,
CB10 1SA, UK. E-mail enquiries: humquery@sanger.ac.uk Clone

requests: clonerequestGeanger.ac.uk

On Nov 20, 2000 this sequence version replaced gi:1117809.

During sequence assembly data is compared from overlapping clones,
Where differences are found these are annotated as variations
together with a note of the overlapping clone name. Note that the
variation annotation may not be found in the sequence submission

corresponding to the overlapping clone, as we submit sequences with
only a small overlap as described above.

The following abbreviations are used to associate primary accession
numbers given in the feature table with their source databases:

Em., EMBL; Sw., SWISSPROT, Tr., TREMBL; Wp., WORMPEP; Information
on the WORMPEP database can be found at
http://www.sanger.ac.uk/Projects/C elagans/wormpep This sequence
was generated from part of bacterial clone contigs of human
chromosome 6, constructed by the Sanger Centre Chromosome 6 Mapping
Group. Further information can be found at
http://www.sanger.ac.uk/HGP/Chr6
IMPORTANT: This sequence is not the entire insert of clone
RP11-203Hz It may be shorter because we sequence overlapping
sections only once, except for a 100 base overlap.
The true left end of clone RP1-328K6 is at 1001 in this sequence.
The true left end of clone RP1-328K6 is at 1001 in this sequence.
The true left end of clone RP1-328K6 is at 100 in this sequence.
The true left end of clone RP1-328K6 is at 100 in this sequence
chemistry or covered by high quality data (i.e., phred quality as
compressions and repeats; all regions were covered by at least
one plasmid subclone or more than one missembly was confirmed by restriction digset. RP11-203Hz is from
the library RPC1-11.1 constructed by the group of Pieter de Jong.
For Eurther details see
                                                                                                                                                                                                                 AL359378 100919 bp DNA linear PRI 09-APR-2001 Human DNA sequence from clone RPI1-203H2 on chromosome 6 Contains an STS and GSSs, complete sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 100919)
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/note="LIME3 repeat: matches 5411. .6155 of consensus"
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/db_xref="taxon:9606"
/chromosome="6"
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/clone lib="RPCI-11.1"
110. .277
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Location/Qualifiers
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Direct Submission
                               481 ATGATTTTYACCC 493
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12687. .13148
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/note="match: GSS: Em:B82645"
4413. .4740
                                                                                                                                                                                                                                  32387. .33129
/note="AluJo repeat: matches 1. .296 of consensus" 3333. .33573. .33573 // start and the start and the start and the start and start and
                                                                                                                                                                                                                                                          note="LTR44 repeat: matches 1.
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| note="30 copies 2 mer at 83% conserved
| 0704. .10741
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| note="21 copies 2 mer cc 78% conserved"
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/note="LTR32 repeat: matches 15. .471 of consensus"
7809. .7895
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        note="AluJb repeat: matches 5. .312 of consensus"
                                                                                                                                                                               note="LTR1 repeat: matches 2. .785 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               note="L1MC3 repeat: matches 7026. .7693 of consensus"
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| note="15 copies 2 mer ac 100% conserved
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              note="AluSg1 repeat: matches 1. .300 of consensus"
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184. .8463
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                                                                                                                                                                                                                                                                                                              note="MLT1A1 repeat: matches 10. .365 of consensus" 1883. .32342
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     note="AluSx repeat: matches 1. .182 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                      note="L1MD2 repeat: matches 5830. .6070 of consensus" 0131. .30479
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  note="L1MA6 repeat: matches 3324. .4338 of consensus"
8879. .21256
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             note="L1MD2 repeat: matches 5284. .5830 of consensus"
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2550. .12595
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ote="AluSq repeat: matches 1. .313 of consensus"
|311. .28547
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ote="L1MD2 repeat: matches 5031. .5268 of consensus"
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55. .22057
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3. .27220
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3. .22367
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2. .26553
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                                                                                                                                                                                                                                                                  .490 of consensus"
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Best Local Similarity Matches 97; Conserv
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361 ATCTTCATCCAATGCTAGATTTCATAACTCTTGGATCCTTCTATGTTTTTCAAGTGT 420
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               51187. .51345
/note="LIPA16 repeat: matches 5913.
complement (51373. .51986)
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/note="LIPA10 repeat: matches 5719. .6158 of consensus"
complement(41095. .41838)
/note="match: GSS: Em:AQ374227"
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36453: .36763
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        note="AluSq repeat: matches 1. .294 of consensus" 6682. .47334 note="L2 repeat: matches 1197. .1913 of consensus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        note="AluY repeat: matches 1. .310 of consensus" 3832. .44317
                                                                                                                                                                                                                                                                   note="match:
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3193. .53499
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8086. .48137
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7366. .37399
note="17 copies 2 mer gt 88% conserved"
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3173. .53610
                                                                                                                                                                                                                                                                                                                                                                                                                    note="MIR repeat: matches 150.
1634. .51930
note="AluSx repeat: matches 1.
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                                                                                                                                                                                                                                                                                                         note="L2 repeat: matches 2267.
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1008. .51118
note="MIR repeat: matches 53. .165 of consensus"
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                                                                                                                                                                                                                                                                                       575. .53969
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3857. .46065
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.ote="MER5A repeat: matches 2. .189 of
                                                                                                                                                      50.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 s="L2 repeat: matches 1474. .2083 of
3. .50545
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DDG Joint Genome Institute.
Direct Submission
Submitted (09-UNN-2001) Production Sequencing Facility, DOE Joint
Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA
3 (Dases I to 168575)
DDE Joint Genome Institute and Stanford Human Genome Center.
Direct Submission
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DOE Joint Genome Institute and Stanford Human Genome Center.

Direct Submission

Unpublished
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                                                   421 ATAATTAGAGAGATGCATGGATATATAATAAATAAGTAAAAGCTACGGTATCACCATGTG 480
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                                                                                                                                                                                                                           AC091989 168575 bp DNA linear PRI 30-AUC
Homo sapiens chromosome 5 clone RP11-76H13, complete sequence.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       www-shgc_stanford.edu
Quality: Phrap Quality >=40 99.8% of Sequence;
Estimated Total Number of Errors is 0.2.
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Matches 76; Conservative
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                                                                                                                        42247 ATTTTGTCCACC 42258
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Direct Submission
Submitted (15-APR-2002) Genoscope - Centre National de Sequencage :
BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr
IMPORTANT: This sequence is unfinished and does not necessarly represent the correct sequence.
Work on the sequence is in progress and the release of this data is based on the understanding that the sequence may change as work continue. The sequence may be contaminated with foreign sequence from E.coli, yeast, vector, phage, etc.
The nucleotide sequence of this BAC clone was generated by combining Monsanto and Genoscope sequencing data.
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     HTG 15-APR-2002
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1 (bases to 110913)
Choisne, N., Orjeda, G., Cattolico, L., Demange, N., Wincker, P., Weissenbach, J. and Quetier, F., Scarpelli, C., Salanoubat, M., Orjeda, G., Cattolico, E., Belletier, F., Saranoubat, M., Cattolico, E., Salanoubat, M., Cattolico, E., Salanoubat, M., Cattolico, E., Salanoubat, M., Cattolico, E., Salanoubat, M., Cattolico, E., Cattolico, E., Salanoubat, M., Cattolico, E., Cattolico, 
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Location/Qualifiers
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                                           Oryza sativa chromosome 12 clone Monsanto-001494 F10, SEQUENCING IN PROGRESS ***, in ordered pieces.
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10497 bp contig from 1 to 10497
2346 bp contig from 10596 to 12943
3998 bp contig from 13044 to 13041
15976 bp contig from 13142 to 33117
24871 bp contig from 33218 to 58088
1124 bp contig from 58189 to 58088
1124 bp contig from 58189 to 59319
4909 bp contig from 59420 to 84328
26488 bp contig from 94420 to 109913.
* NOTE: This is a "working draft" sequence.
* This sequence will be replaced
DNA
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22828 c 22735 g 32434 t
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                                                                                                                                                                                            AL713902.1 G1:19701072
HTGS PHASE2; HTGS_ACTIVEFIN.
Oryza sativa
Oryza sativa
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/sub_species="japonica"
/db_xref="taxon:4530"
110913 bp
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2 (bases 1 to 110913)
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ses 95; Conservative
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Db 119093 ATGGGTGT 119086

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Best Local Similarity
Thes 95; Conserve
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                                          Db 119153
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BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr
- Web : www.genoscope.cns.fr)
IMPORTANT: This sequence is unfinished and does not necessarly
represent the correct sequence.
Work on the sequence is in progress and the release of this data is
based on the understanding that the sequence may change as work
continue. The sequence may be contaminated with foreign sequence
from E.coli, yeast, vector, phage, etc.
* NOTE: This is a 'working draft' sequence.
* This sequence will be replaced

* by the finished sequence as soon as it is available and

* the accession number will be preserved.
ATGGATAT 444
                                      AAAATACATGACTAACTGAACCGTAAATTATAATAGTACTGTAGTGAATTAAAGATATCT 119094
                                                                          ATGGATAT 444
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Oryza sativa chromosome 12 sequencing
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Spermatophyta; Magnoliophyta; Liliopaida; Poales; Poaceae;
Ehrhartoideae; Oryzae; Oryza.
1 (bases 1 to 137936)
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/sub_species="japonica"
/db_xref="taxon:4530"
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/clone_lib="OSJNBa"
29563 c 29308 g 40105 t
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                                                                                                                                                                                                                                                                                             8.0%; Score 39.2; DB 2;
50.5%; Pred. No. 5.6;
Stive 0; Mismatches 93;
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ORGANISM
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Bource
                                           377 AGATTTCATAACTCTTGGATCCATCTTCTATGTTTTTCAAGTGTATAATTAGAGAGATGC 436
AAAATACATGACTAACTGAACCGTAAATTATAATAGTACTGTAGTGAATTAAAGATATCT 125935
                                                                                                                                      TTGGGTCCAGTGCCAGGGCATGCAACCCTTTTGGTTGGAAGAGTATCTTCATCCAATGCT 376
                                                                                                                                                                                                                                                                                 95;
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933 bp contig from 2063 to 2995
938 bp contig from 3996 to 4578
2449 bp contig from 5579 to 8027
66895 bp contig from 9028 to 75922
67856 bp contig from 76923 to 144778.
* NOTE: This is a 'working draft' sequence.
* NOTE: This is a 'working draft' sequence.
* This record will be updated with the finished sequence
* as soon as it is available and the accession number will
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Work on the sequence is in progress and the release of this data based on the understanding that the sequence may change as work continue. The sequence may be contaminated with foreign sequence from E.coli, yeast, vector, phage, etc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Direct Submission

Submitted (06-FEB-2001) Genoscope - Centre National de Sequencage :

BP 191 91006 EVRY cedex - FRANCE (B-mail : seqref@genoscope.cns.fr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Salse, J., Choisne, N., Orjeda, G., Regad, F., Lorieux, M., Delseny, M., Robert, C., Brottier, P., Wincker, P., Cruaud,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzeae; Oryza.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Oryza sativa.
Oryza sativa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Oryza sativa chromosome 12 clone OSJNBa0041K23, *** PROGRESS ***, in unordered pieces.
                                                                                                                                                                                                                                                                                                    Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Contigs composition
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                IMPORTANT: This sequence is unfinished and does not necessarly
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Genoscope.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Unpublished
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Oryza sativa chromosome 12 sequencing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Artiguenave, F., Saurin, W., Salanoubat, M., Quetier, F. and Weissenbach, J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               HTG; HTGS_PHASE1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CNS07EFR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               represent the correct sequence.

    Web : www.genoscope.cns.fr)

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                                                                                                                                                                                                                                                                                                                                                                                               40362
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             be preserved
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (bases 1 to 144778)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (bases 1 to 144778)
                                                                                                                                                                                                                                                                                 Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                           /organism="Oryza sativa"
/cultivar="Nipponbare"
/sub_species="japonica"
/db_xref="taxon:4530"
/chromosome="12"
                                                                                                                                                                                                                                                                                                                                                                                        /clone="0SJNBa0041K23"
/clone_lib="CUGI Nipponbare BAC"
30027 c 29723 g 39633 t 5033 others
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1. .144778
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Location/Qualifiers
                                                                                                                                                                                                                                                                                                    50.5%;
                                                                                                                                                                                                                                                                              0
                                                                                                                                                                                                                                                                                                    Score 39.2;
Pred. No. 5.
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                                                                                                                                                                                                                                                                              Mismatches
                                                                                                                                                                                                                                                                                                                            88
                                                                                                                                                                                                                                                                              93;
                                                                                                                                                                                                                                                                                                                    Length 144778;
                                                                                                                                                                                                                                                                              Indels
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BASE COUNT
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JOURNAL
REFERENCE
AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ACCESSION
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KEYWORDS
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AC090757
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                                                                                                                                                                                                                                                                                                           FEATURES
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Submitted (28-APR-2000) Masahira Hattori, The Institute of Physical Submitted (28-APR-2000) Masahira Hattori, The Institute of Physical Submitted (28-APR-2000) Masahira Espace (28-855, Sitasato Univ., 1-15-1 Kitasato, Sagamihara, Kanagawa 228-855, Japan (E-mail:hattori@gec.riken.go.jp, Tel:81-42-778-9923, Pax:81-42-778-9924)
On May 30, 2000 this sequence version replaced gi:7678794.
Center: RIKEN Genomic Sciences Center (GSC)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NOTE: This is a 'working draft' sequence. It currently consists of 6 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be
                                                                                                                                                                                               HTG 30-MAY-2000
                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota, Metazoa; Chordata, Craniata, Vertebrata; Buteleostomi; Mammalia; Butheria; Primates; Catarrhini, Hominidae; Homo.

I bases I to 152137)

Hattori,M. 1shi,K. Toyoda,A., Taylor,T.D., Hong-Seog,P., Fujiyama,A., Yada,T., Totoki,Y., Watanabe,H. and Sakaki,Y. Published Only in Database (2000)

2 (bases I to 152137)

2 (bases I to 152137)

Publishama,A., Yada,T., Totoki,Y., Watanabe,H. and Sakaki,Y. Pujiyama,A., Yada,T., Totoki,Y., Watanabe,H. and Sakaki,Y. Direct Submission
                                                                                                                                                  152137 bp ' DNA linear HTG 30-MAY-Homo sapiens chromosome 18 clone RP11-701G2 map 18q22, WORKING AP001932
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Web site: http://hgp.gsc.riken.go.jp/
Contact: hattori@gsc.riken.go.jp/
Contact: hattori@gsc.riken.go.jp/
Contact: hattori@gsc.riken.go.jp/
Center project name: Humbraft18
Center project name: RP11-70162
Center clone name: RP11-70163
Center clone name: RP11-70163
Assembly program: Phrapy version 0.99039
Consensus quality: 146725 bases at least Q30
Consensus quality: 146725 bases at least Q30
Consensus quality: 150929 bases at least Q20
Insert size: 151637; sum-of-contigs
Quality coverage: 6.40x in Q20 bases; sum-of-contigs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                * arbitrary. Gaps between the contigs are represented as * runs of N, but the exact sizes of the gaps are unknown. * This record will be updated with the finished sequence * as soon as it is available and the accession number will
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         34616 bp in length
38989 bp in length
29414 bp in length
26510 bp in length
14781 bp in length
7327 bp in length
                                                                                                                                                                                                                                                                                                              AP001932.2 GI:8117579
HTG; HTGS_PHASE1; HTGS_DRAFT.
Homo sapiens DNA, clone:RP11-701G2.
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                                                     Db 125934 ArddGrer 125927
                                                                                                                                                                                                                                                                                                                                                                                                           Homo sapiens
437 ATGGATAT 444
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                                                                                                                                                                                                                                                                                                                                                                       SOURCE
                                                                                                                                                                                                                                DEFINITION
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REFERENCE
                                                                                                                                                                                                                                                                                         ACCESSION
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              REFERENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AUTHORS
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                                                                                                                                                                       AP001932
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TITLE

TITLE

VERSION

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Diren, Bartier, W. Bastier, L. Musbaum, C., Lander, E., Allen, N., Anderson, S., Barren, B., Linton, L., Nusbaum, C., Lander, E., Allen, N., Anderson, S., Barren, M., Bastien, V., Boguslavkiy, L., Boukhgalter, B., Brown, A., Comarata, J., Campopiano, A., Choepel, Y., Colangelo, M., Collins, S., Collymore, A., Cooke, P., DeArellano, K., Dewar, K., Diaz, J.S., Dodge, S., Farco, S., Ferreira, P., FitzHugh, W., Gage, D., Galagan, J., Gardyna, S., Ginde, S., Goyette, M., Graham, L., Grand-Pierre, N., Jahagos, B., Heaford, A., Horton, L., Hulme, W., Iliev, I., Johnson, R., Jones, C., Karatas, A., LaRocque, K., Lamazares, R., Landers, T., Lehoczky, J., Levine, R., Liu, G., MacLean, C., Macdonald, P.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            153485 bp DNA linear HTG 24-MAY-2001
Homo sapiens chromosome 18 clone RP11-701G2 map 18, WORKING DRAFT
SEQUENCE, 1 ordered piece.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 153485)

Birren, B., Linton, L., Nusbaum, C. and Lander, E.

Homo sapiens chromosome 18, clone RP11-70162
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /noce="assembly_fragment"
73806. .103219
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103320. .129829
/noce="assembly_fragment"
129930. .144710

    .34616
/note="assembly_fragment clone_end:T7 vector_side:right"
34717. .73705

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                34616: contig of 34616 bp in length
34617 34716: gap of 100 bp
34717 73705: contig of 38989 bp in length
73706 73805: gap of 100 bp
73806 103219: contig of 29414 bp in length
103220 103319: gap of 100 bp
103320 129929: contig of 26510 bp in length
129830 129929: gap of 100 bp
129330 144710: contig of 14781 bp in length
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                                                                                                                                                                                                                                                                                                   144711 144810: gap of 100 bp 144811 152137: contig of 7327 bp in length. Location/Qualifiers
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HTG; HTGS PHASE2; HTGS_DRAFT; HTGS_FULLTOP.
Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DD 59448 TATATATACATATATACATGTATATATATATA 59482
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /note="assembly_fragment"
144411. 152137
/note="assembly_fragment"
49625 a 26249 c 26522 g 49241 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Pest Local Similarity 63.2%; Pred. No. 6.3;
Best Local Similarity 63.2%; Pred. No. 6.3;
                                                                                                                                                                                                                                                                                                                                                                                                                                     organism="Homo sapiens"
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/chromosome="18"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /clone="RP11-701G2"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /map="18q22"

    be preserved.

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Db 103951 TATATATACATATACATGTATATATATATATA 103985
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                                                                                                                                                                                                                                                                                                                            Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Bource
                                                                                                                                                                                                                                                                                               Local
                                          TATAATTAGAGAGATGCATGGATATAATAAATA 454
                                                                                                                   60;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       assembly_fragment
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                                                                                                                                                                                                                                                                                               Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    http://ftp.genome.washington.edu/RM/RepeatMasker.html
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NOTE: This is a 'working draft' sequence. It currently consists of 1 contigs. Gaps between the contigs are represented as runs of N. The order of the pieces is believed to be correct as given, however the sizes of the gaps between them are based on estimates that have provided by the submittor.

This sequence will be replaced by the finished sequence as soon as it is available and the accession number will be preserved.

1 153485: contig of 153485 bp in length.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Insert size: 155000; agarose-fp
Insert size: 153485; sum-of-contigs
Quality coverage: 9.5 in Q20 bases; agarose-fp
Quality coverage: 9.6 in Q20 bases; sum-of-contigs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequencing vector: Plasmid; nd; 100% of reads Sequencing vector: Plasmid; nd; 100% of reads Chemistry: Dye-terminator Big Dye; 100% of read Assembly program: Phrap; version 0.960731 Consensus quality: 15323 bases at least Q30 Consensus quality: 153480 bases at least Q30 Consensus quality: 153480 bases at least Q30 Consensus quality: 153480 bases at least Q30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Center project name: L12250 Center clone name: 701_G_2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Contact: sequence_submissions@genome.wi.mit.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ------ Genome Center
Center: Whitehead Institute/ MIT Center for Genome Research
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Web site: http://www-seq.wi.mit.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Center code: WIBR
                                                                                                                                                                                                                                                              Conservative
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/clone_lib="RPCI-11 Human Male BAC"
26340 c 26956 g 49761 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          organism="Homo sapiens"
/db_xref="taxon:9606"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /chromosome="18"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ocation/Qualifiers
                                                                                                                                                                                                                                                                                     7.9%;
                                                                                                                                                                                                                                                                                                                                                                                                               26956 g 49761 t
                                                                                                                                                                                                                                                                                 Score 39; DB
Pred. No. 6.3;
                                                                                                                                                                                                                                                       Mismatches
                                                                                                                                                                                                                                                                                                            DB 2; Length 153485;
                                                                                                                                                                                                                                                       35;
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AUTHORS
TITLE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CE 3 (bases to 17502)

RS Birren, B., Linton, L., Nusbaum, C., Lander, E., Ali, A., Allen, N., Anderson, S., Barna, N., Bastien, V., Boyslavkiy, L., Boukhgalter, B., Anderson, S., Barna, N., Bastien, V., Boyslavkiy, L., Boukhgalter, B., Anderson, S., Barna, N., Bastien, V., Boyslavkiy, L., Boukhgalter, B., Brown, A., Chang, J., Chazaro, B., Choepel, Y., Colangelo, M., Collins, S., Collymore, A., Cooke, P., DeArellano, K., Dewar, K., Diaz, J.S., Dodge, S., Faro, S., Ferreira, P., FitzHugh, W., Gage, D., Galagan, J., Gardyna, S., Ginde, S., Gord, S., Goyette, M., Graham, L., Grand-Pierre, N., Hagos, B., Heaford, A., Horton, L., Hilme, W., Iliev, I., Johnson, R., Jones, C., Kamat, A., Kells, C., LaRocque, K., Lamazares, R., Landers, T., Lehoczky, J., Levine, R., Liu, G., MacLean, C., Macdonald, P., Major, J., Marquis, N., Matthews, C., McCarthy, M., McEwan, P., McKernan, K., McChaeters, R., Meldrim, J., Meneus, L., Mihova, T., Mlenga, V., Murphy, T., Naylor, J., Nguyen, C., Northu, C., Norman, C., H., Murphy, T., Naylor, J., Nguyen, C., Northu, C., Norman, C., Peterson, K., Phunkhang, P., Pierre, N., Pollara, V., Raymond, C., Retta, R., Rieback, M., Riley, R., Schauer, S., Schupback, R., Seaman, S., Severy, P., Sougnez, C., Spencer, B., Stange-Thomann, N., Stojanovic, N., Tavers, M., Trayers, M., Trigilio, J., Vassiliev, H., Viel, R., Vo, A., Wilson, B., Wu, X., Wyman, D., Ye, W.J., Young, G., Zainoun, J., Zembek, L., Zimmer, A. and Zody, M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RS Birren, B., Linton, L., Nusbaum, C., Lander, E., Abraham, H., Allen, N., Anderson, S., Baldwin, J., Barna, N., Beckerly, R., Beda, F., Boduslavkiy, L., Boukhgalter, B., Brown, A., Burkett, G., Castle, A., Choepel, Y., Colangelo, M., Collins, S., Collymore, A., Cooke, P., DeArellano, K., Dewar, K., Domino, M., Doyle, M., Fenestor, J., Ferreira, P., Fitzhugh, W., Forrest, C., Gage, D., Galagan, J., Gardyna, S., Crant, G., Hagos, B., Heford, A., Horton, L., Karatas, A., Klein, J., Gardyna, S., Crant, G., Jones, C., Kann, L., Karatas, A., Klein, J., Gardyna, S., T., Lehoczky, J., Levine, R., Lieu, C., Liu, G., Looke, K., Macdonald, P., Marquis, N., McEwan, P., McGurk, A., McKernan, K., McDeeters, R., Meldrim, J., Meneus, L., Morrow, J., Naylor, J., Norman, C.H., O'Connor, T., O'Donnell, P., Olivar, T. M., Peterson, K., Pierre, N., Pisani, C., Pollara, V., Raymond, C., Riley, R., Rothman, D., Spencer, B., Stange-Thomann, N., Soloramonic, N., Subramanian, A., Talamas, J., Tesfaye, S., Theodore, J., Tirrell, A., Vassilitev, H., Viel, R., Vo, A., Wu, X., Wyman, D., Ye, W.J.,
                                                                                                                                                                                                                    Submitted (29-JUN-2001) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA On Jun 28, 2001 this sequence version replaced gi:14190661. All repeats were identified using RepeatMasker: Smit, A.F.A. & Green, P. (1996-1997) http://ftp.genome.washington.edu/RM/RepeatMasker.html
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Research, 320 Charles Street, Cambridge, MA 02141, USA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Direct Submission
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Birren, B., Linton, L., Nusbaum, C. and Lander, E.
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Contact: sequence_submissions@genome.wi.mit.edu------ Project Information
                                                                                 Web site: http://www-seq.wi.mit.edu
                                                                                                                          Center: Whitehead Institute/ MIT Center for Genome Research Center code: WIBR
                                                                                                                                                                                               -- Genome Center
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/rpt family="LiME1"
complement(18230. .18722)
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Center clone name: 510_D_19
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                                                                                                                          clone="RP11-510D19"
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9260. 9551
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4338 . 4336

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2782. 32888
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complement (37388. 377,
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                                                                                                 Submitted (13-JUL-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA
On Jul 12, 2002 this sequence version replaced gi:18141352.

Center: Baylor College of Medicine
Center code: BCM
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arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number wil
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NOTE: This is a 'working draft' sequence. It currently consists of 47 contigs. The true order of the pieces is not known and their order in this sequence record is
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Chemistry: Dye-terminator Big Dye: 100% of reads
Assembly program: Phrap; version 0.990329
Consensus quality: 54814 bases at least Q40
Consensus quality: 59343 bases at least Q30
Consensus quality: 63485 bases at least Q20
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119 9218: contig of 9118 bp in length

129 9218: gap of unknown length

1219 17046: contig of 7828 bp in length

17146: gap of unknown length

17147 34899: contig of 17733 bp in length

1900 34999: gap of unknown length

1900 57107: gap of unknown length

1008 57107: gap of unknown length

1008 14976: contig of 92660 bp in length

1008 14976: contig of 92660 bp in length.
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/organism="Felis catus"
/db_xref="taxon:9685"
/clone="RP86-252E8"
/clone_lib="RP86"
                                                                                                      AC113238
AC113238.1 GI:18958665
HTG: HTGS_PHASE1; HTGS_DRAFT.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Unpublished
2 (bases 1 to 149767)
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RESULT 11
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contig of 2730 bp in length
gap of unknown length
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gap of unknown length
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contig of 2097 bp in length
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unknown length
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83381: gap of unknown length
87785: contig of 4404 bp in length
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94967: gap of unknown length
99862: contig of 4895 bp in length.
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gap of unknown leng
contig of 2442 bp i
gap of unknown leng
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gap of unknown l
contig of 3290 b
contig of 2737 b
gap of unknown l
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gap of unknown
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/clone="CH230-134K22"
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80414: gap of unk
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Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Bukaryota; Butheria; Carnivora; Fissipedia; Felidae; Felis.

1 (bases 1 to 149767)

8 Akhter, N., Ayele, K., Beckstrom-Sternberg, S.M., Benjamin, B., Blakealey, R.W., Bouffard, G.G., Breen, K., Brinkley, C., Brooks, S., Dietrich, N.L., Granite, S., Guan, X., Gupta, J., Haghighi, P., Ho, S.-L., Idol, J.R., Karlins, E., Laric, P., Lee-Lin, S.-Q., Mastrian, S.-D., McCloskey, J.C., McDowell, J., Pearson, R., Prasad, A., Stantripop, S., Thomas, J.W., Thomas, P.J., Touchman, J.W., Tsurgeon, C., Vogt, J.L., Walker, M.A., Wetherby, K.D., Wiggins, L., Young, A., Zhang, L.H. and Green, E.D.
AC113238 149767 bp DNA linear HTG 27-FEB-2002
Felis catus clone RP86-252E8, WORKING DRAFT SEQUENCE, 5 unordered
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Submitted (27-FEB-2002) NIH Intramural Sequencing Center, 8717
Grovemont Circle, Gaithersburg, MD 20877, USA
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Center clone name: 252E08

Sequencing vector: plasmid; n/a: 100% of reads
Sequencing vector: plasmid; n/a: 100% of reads
Chemistry: Dye-terminator Big Dye; 100% of reads
Assembly program: Phrap; version 0.990319
Consensus quality: 147596 bases at least Q40
Consensus quality: 147747 bases at least Q20
Insert size: 135000; agarose-fp
Insert size: 149367; sum-of-contigs
Quality coverage: 10.56% in Q20 bases; sum-of-contigs
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REFERENCE
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                                                                                                                                                                                        Submitted (29-MAR-2002) Genome Analysis, Institute of Molecular Biotechnology, Beutenberstr. 11, Jena 07745, Germany CDS predictions from GenelD may contain errors. Further Information is available from IMB Jena, Department of Genome Analysis (http://genome.imb-jena.de/dictyostelium/) and the Univerity Colonge, Institute for Biochemistry I (http://www.uni-koeln.de/dictyostelium/project.shtml
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          80;
                                                                                                                                                                                                                                                                                                                                                                                                                                   Gloeckner,G., Eichingér,L., Szafranski,K., Pachebat,J., Dear,P., Lehmann,R., Baumgart,C., Parra,G., April,J.F., Guigo,R., Kumpf,K. Tunggal,B., Cox,E., Quail,M.A., Platzer,M., Rosenthal,A. and Noegel,A.A.
                                                                                                                                                                               Funding
                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence and Analysis of Chromosome 2 of Dictyostelium
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Dictyostelium discoideum.
Dictyostelium discoideum
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Gloeckner, G., Eichinge
                                                                                                                                                                                                                                                                                                                              Direct Submission
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                                                                                                                      gency : Deutsche Forschungsgemeinschaft (DFG)
NOTE: This is a 'working draft' sequence.
This sequence will be replaced
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                                                                                                                                                                                                                                                                                                                                                                               Dictyostelium Genome Sequencing Consortium
                                                                                                                                                                                                                                                                                                                                                 gart
                                                                                  the finished sequence as soon as it is available and accession number will be preserved.
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57108. .149767
                                                                       Location/Qualifiers
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SNSQLLLSSSSDSAIKESTTISTSTSTSTSTSTSPSISPSLENSTLSPRNMNTQTSS
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                                                                                                                                                                                     SDVIIPIKGPKGNASILFNLYASDDKWQVRNAEVIFNSDNKKKQIIKATSDQL"
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PEWTHVSEHAKAFIRNLIVKDPDQRHTAKQCLDDLWLSGSDQSIGSAADLHSHFAEKM
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complement(join(8224. .9460,95.
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complement(join(5120. .5211,5342. .6798,6919. .733)
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'codon start-1
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DEEYFADFCLCNPPFFKDLNENNNKNNPKSNCTGSVNEMVTDGGEFFFVKRIIKES
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INNINNINNINNINNINNINNINNINKIVEI IKLILDINDI IYKTDENIIKYECKYLLANV
IVGSSIKLDRDI EFLFTIFIDLTTRLILFKPIDPKINNINNINNINNINNINNINNINNIN
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SIRKFLSIIISVIYFNNHFTSLLFTGTILVFLGTFMYSTSGKVIEKPLPPTKQVKEIE
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FATVAFISFPVNIRWKQVFSIFWIPIGLRERKIPLKTYFLMVSIFFILSVLNNKALDC
DIPIPFHMIFRSSSLLSTIVIGSIFYRKSYSKQQILSLIMVTLGIIFATFSSMPDSKK
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TQTSTLWQTVSLPPILPNEQYYLEYFLSSQFETNINPVLNVYVDNRPVASYNGNLLLG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /translation="MKILLTFILLINLIIVKSDLVVKTNVYNSPGCTGGVNKTVLHSH
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hote="ORF ID:dd_00653"
/codon_start=1
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                                                                                                                                                                                                                                                                                                                                                                                   complement (23858. .24619)
/note="ORP_ID:dd_00658"
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/product=hypothetical protein"
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/protein_id="AAL99331.1"
/db_xref="G1:19807762"
xref="GI:19807760"
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SOS

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Direct Submitted (13-MAR-2001) Sanger Centre, Hinxton, Cambridgeshire, Cubmitted (13-MAR-2001) Sanger Centre, Hinxton, Cambridgeshire, CB10 1SA, UK. E-mail enquiries: humquery@sanger.ac.uk Clone crqueests: clonerquest@sanger.ac.uk

On Mar 11, 2001 this sequence version replaced gi:12961937.

During sequence assembly data is compared from overlapping clones. Where differences are found these are annotated as variations together with a note of the overlapping clone name. Note that the variation annotation may not be found in the sequence submission corresponding to the overlapping clone, as we submit sequences with only a small overlap as described above.

This sequence was finished as follows unless otherwise noted: all regions were either double-stranded or sequenced with an alternate chemistry or covered by high quality data (i.e., phred quality) as compressions and repeats; all regions were covered by at least one plasmid subclone or more than one M13 subclone; and the assembly was confirmed by restriction digest. The following abbreviations are used to associate primary accession numbers given
                                                                                                                                                                                                                                     GRSKRNKTEQYLKEWVASNGNQKRERLEDSIPDLPENREARBFLRNAPTKGLHQPLGK
EVVNQCWKCKFYGHAALECTQTNP FASTKLKKREDEMIQYNDHDDFGENNNKNNIN
INNINNINNIN THKDRI INKINTNDENIDNINKWIKKQKKLKQLQELLARAERIERKRK
EKKRKKKKKKKTKASKKSHHRHSSDSDSGGGSSDSDSDLSKDESYSSNESE"
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Human DNA sequence from clone RPI1-326D19 on chromosome 13,
                                                                                                                                    /trānslation="MDRRDYSKEKYKYGDNDKDRRFSNDKIRHNFDEFTMPSNDRRDR
DKDIDRYRDRYRDRYRDRDRDRDRDRDRDRBRERERERERERSRSPNRNYSRNNNSSS
                                                                                                                                                                                                     YNSNNSSSSFDDGYKYRDMDRERDKYRENKRFDSSRNNEDHRSSIRPLSYDGYDDDDY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 159919)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  in the feature table with their source databases: Em:, EMBL; Sw:, SWISSPROT; Tr:, TREMBL; Wp:, WORMPEP; Information on the WORMPEP database can be found at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               http://www.sanger.ac.uk/Projects/C_elegans/wormpep This sequence was generated from part of bacterial clone contigs of human chromosome 13, constructed by the Sanger Centre Chromosome 13
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     'product="Putative Acyltransferase"
                                                                                                                                                                                                                                                                                                                                                                  join(39790. .40108,40252. .47744)
/note="ORF ID:dd_01572"
/codon_start=1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         7.8%; Score 38.4; DE 56.2%; Pred. No. 9.4;
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                                                            'protein_id="AAL99333.1"
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                                                                                             db_xref="GI:19807764"
codon_start=1
/product="PAP-1.
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CDS

/note="ORF_ID:dd_01574"

FEATURES

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           pping Group. Further information can be found at tp://www.sanger.ac.uk/HGP/Chrl3
11-326D19 is from the library RPCI-11.2 constructed by the Pieter de Jong. For further details see
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           sequence is the entire insert of clone RP11-326D19 The t end of clone RP11-229I7 is at 61034 in this sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             7769. .7996
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|db_xref="taxon:9606"
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                                                                         23694. .23996
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                                                                                    note="L1M4 repeat: matches 3310. .3360 of consensus"
3303. .23693
TOCE="THEIC repeat: matches 1. .371 of consensus"
                                                                                                                                                                                                                                                                                                                                                        note="18 copies 2 mer tt 86% conserved"
10660. .21162
note="L1MB8 repeat: matches 5649. .6161 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      note="AluJo repeat: matches 93. .282 of consensus"
,6400. .16453
,note="27 copies 2 mer ta 77% conserved"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           note="
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   note="30 copies 2 mer at 75% conserved"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   clone_lib="RPCI-11.2"
                           note="L1M4 repeat: matches 3074. .3310 of consensus" 4000. .24037
                                                                                                                                                                              note="MLT1A1 repeat: matches 1.
                                                                                                                                                                                                                                                                   note="21 copies 4 mer gaag 77% conserved"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       note="L1MD2 repeat: matches 5638. .6094 of consensus"
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                                                                                                                                                                                                                          note="L1M4 repeat: matches 3360. .4073 of consensus"
                                                                                                                                                                                                                                                                                               2022. .22105
                                                                                                                                                                                                                                                                                                                 note="L1 repeat: matches 4045. .4250 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  note="L1MD2 repeat: matches 5491. .5638 of consensus'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           note="AluSp repeat:
3830. .13977
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         copies 2 mer tt
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         81% conserved'
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/note="LIPA3 repeat: matches 5378. .6146 of consensus"
25498. .26057
      /note="L1M4 repeat: matches 4110.
52868. .52899
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        28572. .28675
/note="L2 repeat: matches 210. .314 of consensus"
29376. .3119
/note="L1 repeat: matches 3165. .4993 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        26649. .26903
/note="AluSg repeat: matches 1. .255 of consensus"
27125. .27152
/note="7 copies 4 mer atag 92% conserved"
27432. .27509
                                                51893. .52011
                                                                                                                                                                                     49989. .50162
/note="HERVL40 repeat: matches 5352. .5530 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                43968. .43995
/note="7 copie
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45756. .45854
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/note="MER58A repeat: matches 51.
14979. .45156
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/note="THE1C r
36028. .36144
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         note="L2 repeat: matches 332. .510 of consensus" 5044. .35456 note="MLT2FB repeat: matches 1. .413 of consensus"
                                                                    note="AluSg/x repeat: matches 129. .302 of consensus"
                                                                                                                                       0613. .50815
                                                                                                                                                     note="LTR40b repeat:
                                                                                                                                                                                                                                                                     note="HERVL40 repeat: matches 1380. .1617 of consensus" 6979. .49348
                                                                                                                                                                                                                                                                                                                                   5888. .46113
note="HERVL40 repeat: matches 1124. .1351 of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   note="MIR repeat: matches 20. .141 of consensus" 9167. .39460
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         note="MER44 repeat: matches 474.
2405. .32952
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 note="19 copies 2 mer aa 78% conserved"
1773. .31867
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             note="MADE1 repeat: matches 8. .80 of consensus"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          note="50 copies 2 mer gt 68% conserved"
7595. .37800
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2954. .33113
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                                                                                                              note="L2 repeat: matches 2535.
                                                                                                                                                                                                                                                                                                                                                                               note="LTR41 repeat: matches 3. .102 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1933. .42581
note="MER67C repeat: matches 1. .709 of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              note="AluSx repeat: matches 9. .312 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   note="L2 repeat: matches 2082. .2310 of consensus"
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e="HERV16 repeat: matches 2566. .2674 of consensus"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     copies 4 mer tgtg 96% conserved"
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                                                                                                                                                       matches 4. .458 of
                                                                                                                .2748 of consensus"
                           .4231 of consensus
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During sequence assembly data is compared from overlapping clones. Where differences are found these are annotated as variations together with a note of the overlapping clone name. Note that the variation annotation may not be found in the sequence submission corresponding to the overlapping clone, as we submit sequences with only a small overlap as described above.

This sequence was finished as follows unless otherwise noted: all regions were either double-stranded or sequenced with an alternate chemistry or covered by high quality data (i.e., phred quality >= 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by at least one plasmid subclone or more than one M13 subclone; and the assembly was confirmed by restriction digest. The following
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Actinopterygii; Neopterygii; Teleostei; Ostariophysi;
Cypriniformes; Cyprinidae; Danio.
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HTG; Ca2+ dependent activator; CpG island; fez; forebrain; OGFR;
opioid growth factor receptor; transposon; zinc-finger protein.
zebrafish.
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                                                                                                                                                                                                                                                                                           note="LIMA9 repeat: matches 5549. .6270 of consensus"
                                                                                                                                                                                                                                                                                                                  62138. .62198 ...
/note="LIMA9 repeat: matches 5317. .5375 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /note="L1MA9 repeat: matches 4826. .5309 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  360 TAICTICAACCAATGCTAGATITCATAACTCTTGGATCCATCTTCTATGTTTTTCAAGTG 419
/note="16 copies 2 mer gt 93% conserved"
54804. 54928
/note="L2 repeat: matches 1714. .1838 of consensus"
55708. .55771
                                                                                                                                                                                                                               'note="LTR33 repeat: matches 48. .398 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  note="FLAM A repeat: matches 2. .131 of consensus" 2687. .63166
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              420 TATAATTAGAGAGATGCATGGATATATAATAAATAAGTAAAAGCTACGGTATCACCATGT
                                                                                                                                                                                                                                                                                                                                                                                     52235. .62544
'note="AluY repeat: matches 1. .308 of consensus"
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                                                                                                                                                            note="16 copies 4 mer tatg 78% conserved"
18435. .58781
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abbreviations are used to associate primary accession numbers given in the feature table with their source databases: Em:, EMBL; Sw., SWISSPROT; Tr., TREMBL; Wp:, WORMPEP; Information on the WORMPEP database can be found at
                                                                                                                                                                                                                                                                                                                                           Repeat names beginning 'Dr' were identified by the Recon repeat discovery system (Zhirong Bao and Sean Eddy, submitted), and those beginning 'dr' were identified by Rick Waterman (Stephen Johnson lab, WashU). For further information see http://www/Projects/D_rerio/fishmask.shtml his clone was isolated from a PAC library (Incyte Genomics, Inc.) and provided by G. Levkowitz (Genetech Inc., San Francisco, USA). This sequence is the entire insert of clone BUSM1-6A2 The true left end of clone BUSM1-13 is at 44958 in this sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ACACACTGCATATACATATAAACTTGATGCATGCAAACAC 149% conserved"
2841. .2852
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1338. 1405
/note="Dr000340 repeat: matches 120. 187 of consensus"
                                                                                                 http://www.sanger.ac.uk/Projects/C_elegans/wormpep BUSM1-6A2 is
from a Zebrafish PAC library
VECTOR: pCYPAC-6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               note="3.4 copies 14 mer TACACATACATACA 60% conserved"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  587. .709
/note="1.9 copies 12 mer TACTTAAAATAC 46% conserved"
702. .717
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        158. 477
note="2.0 copies 10 mer AGTTTTACAT 40% conserved"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        note="2.8 copies 9 mer CATTATTAT 34% conserved"
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/note="2.1 copies 9 mer TTGTGACTT 38% conserved"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             note="2.0 copies 8 mer TTAAAATA 32% conserved"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             653. .666
/note="2.0 copies 7 mer TACAAAA 28% conserved"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            806. .822
/note="2.4 copies 7 mer ATAAAAT 25% conserved"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1096. .1107
/note="2.0 copies 6 mer CATACA 24% conserved"
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/note="2.0 copies 6 mer CATATA 24% conserved"
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/note="4.2 copies 4 mer AAAT 34% conserved"
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|hote="2.8 copies 4 mer CATG 22% conserved"
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/note="7.7 copies 3 mer ATT 28% conserved"
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1815. 1826
/note="2.0 copies 6 mer GTCTCA 24% conserv
                                                                                                                                                                                                                Center: Wellcome Trust Sanger Institute
                                                                                                                                                                                                                                                                     Web site: http://www.sanger.ac.uk
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note="4.1 copies 40 mer
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/db_xref="taxon:7955"
/clone="BUSM1-6A2"
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                                                                                                                                                                                                                                                                                                    Contact: zface@sanger.ac.uk
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'note="2.8 c
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                                                                                                                                                                                                                                                                                                                /note="2 ° 6154
                     /note="Tandem repeat. Inconsistency in the number of copies of the repeat element between subclones." 6542. .6575
/note="2.1 copies 16 mer ATTTATCAAAGTGTGA 68% conserv
                                                                                                     complement (6449. .6538)
/note="Dr000340 repeat: matches 117. .207 of consensus"
                                                                                                                                                                                                                            6157. .6187
/note="7.8 copies 4 mer ACAT 62% conserved"
complement(6187. .6391)
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                                                                                                                                            /note="Dr000340 repeat: matches 81. .207 of consensus"
complement(6449. .6538)
                                                                                                                                                                                                    note="Dr000027 repeat: matches 5. .256 of consensus"
                                                                                                                                                                                                                                                                                      /note="2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                             note="
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/note="4.1 copies 40 mer
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complement(4075. .4252)
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Submitted (16-FEB-2002) Genome Sequencing Center, Washington University School of Medicine, 4444 Forest Park Parkway, St. MO 63108, USA
5 (bases 1 to 126118)
Waterston,R.
Direct Submission Submitted (09-MAR-2002) Department of Genetics, Washington
                                                                                                                                     Direct Submission
Submitted (13-DEC-2001) Genome Sequencing Center, Washington
University School of Medicine, 4444 Forest Park Parkway, St.
MO 63108, USA
4 (Dases 1 to 126118)
Waterston, R. H.
Waterston, R. H.
                                                                                                                                                                                                                                                                                 Bielicki,L., Meyer,R., Haglund,K. and Doebber,A.
The sequence of Homo sapiens BAC clone RP11-182K3
Unpublished (2001)
                                                                                                                                                                                                                                                                                                                                                                                      1 (bases 1 to 126118)
Sulston, J. E. and Waterston, R.
Toward a complete human genome sequence
Genome Res. 8 (11), 1097-1108 (1998)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Homo sapiens BAC clone RP11-182K3 from AC104598
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                                                                                                                                                                                                                                               Waterston, R.H.
                                                                                                                                                                                                                                                                                                                                                        9847074
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Homo sapiens
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ilarity 55.7%;
Conservative
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/note="2.0 copies 6 mer CATATA 24% conserved"
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/note="2.0 copies 8 mer TTAAAATA 32% conserved"
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7290. .7312
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /note="2.8 copies 4 mer TTTG 22% conserved"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /Note="1.9 copies 12 mer TACTTAAAATAC 46% conserved"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  note="2.0 copies 7 mer TACAAAA 28% conserved"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        note="2.0 copies 10 mer AGTTTTACAT 40% conserved" 694. .7707
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     note="4.7 copies 3 mer AAT 28% conserved"
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Pred. No. 11;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DB 5;
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complete sequence
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                                                                                                                                                                                              Louis,
                                                                                          Louis,
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note="similar to Bos taurus EST BE810028 (NID:g10241140)"
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                                                 7525. .7604
/note="similar to Bos taurus EST BI680079 (NID:g15632987)"
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13841. 14227
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13884. .14235
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12027. .12481

rpt family="MER2_type"

7.014. .12774

/note="match to EST BG983142 (NID:g14385864)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              //noce="match to EST BE811024 (NID:g10243258)"
10204. 10325
//noce="match to EST BE811026 (NID:g10243260)"
10207. 10361
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/note="match to EST BE811072 (NID:gl0243306)"

10223. 10361

/note="match to EST AL517947 (NID:gl2781440)"

(0319. 10361
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.0204. .10361
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.0204. .10361
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                                                                                                                                                                                                                                                                                                                                                                                                                                           note="match to EST AL517947 (NID:g12781440)"
                                                                                                                                                                                                                                             3473. .8926
/note="match to EST BF935807 (NID:g12353131)"
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/note="match to EST AA328955 (NID:g1981442)"
                           'note="match to EST BI859737 (NID:g16000484)"
                                                                                                                                                                              'note="match to EST AU134477 (NID:g10995016)"
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note="match to EST AL037954 (NID:95407270)"
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10213. 10325
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nocte="similar to Mus musculus EST BB615821
NID:g16456044)"
                                                                                          7525. .7604
/note="similar to Mus musculus EST BB615821
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1736, 12024
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1467. .11735
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13615. :13994
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8473_ .8926
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13162. .13187
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13003. .13026
                                                                                                                                                                                                                                                                                                          /rpt_family="Alu"
9379. .9665
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                                                                                                                                       (NID:916456044)"
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Mapping information for this clone was provided by Dr. John D. McPherson, Department of Genetics, Washington University, St. Louis MO. For additional information about the map position of this sequence, see http://genome.wustl.edu/gsc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The RPCI-11 human BAC library was made from the blood of one male donor, as described by Osoegawa, K., Woon, P.Y., Zhao, B., Frengen, B., Tateno, M., Catanese, J.J. and de Jong, P.J. (1998) An improved approach for construction of bacterial artificial chromosome libraries. Genomics 511-8. The clone may be obtained aither from Research Genetics, Inc. (http://www.resgen.com) or Pieter de Jong
                                                                                                                                                                                                                                                  NOTICE: This sequence may not represent the entire insert of this clone. It may be shorter because we only sequence overlapping clone sections once, or longer because we provide a small overlap between neighboring data submissions.
                                                                                                                                                                                                                                                                                                                                                       This sequence was finished as follows unless otherwise noted: all regions were double stranded, sequenced with an alternate chemistry, or covered by high quality date (i.e., phred quality >= 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by sequence from more than one subclone; and the assembly was confirmed by
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NEIGHBORING SEQUENCE INFORMATION:
The clone sequenced to the left is RP11-252K7, 2000 bp overlap.
Actual start of this clone is at base position 106699 of
RP11-252K7; actual end is at base position 126118 of RP11-182K3.
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/note="match to EST BE811026 (NID:g10243260)"
7525. .7604
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/note="match to EST BE926756 (NID:g10452832)"
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'note="match to EST AL037617 (NID:95928218)"
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note="match to EST AL037954 (NID:95407270)"
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'note="aimilar to Homo sapiens EST BF890821
(NID:912282280)"
                                                                                                                       Web site: http://genome.wustl.edu/gsc
Contact: sapiens@watson.wustl.edu
------ Summary Statistics
                                                                                                                                                                                       Center project name: H_NH0182K03
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /db_xref="taxon:9606"
/chromosome="2"
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1892, ,1918
/rpt_family="(A)n"
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/note="match to EST
7525. .7604
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rpt_family="MaLR"
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Search completed: January 12, 2003, 08:14:38 Job time: 3376 secs
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                                                                                                                                                                                       59800 ATGAATTCAATGTTGAGGCAAAAAAAT 59826
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                                                                                                                                                                                                                                                                                              451 AATAAGTAAAAGCTACGGTATCACCAT 477
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           391 TIGGATCCAICTICTATGTITTTCAAGTGTATAATTAGAGAGATGCATGGATATATAATA 450
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   331 AGGGCATGCAACCCTTTTGGTTGGAAGAGTATCTTCATCCAATGCTAGATTTCATAACTC 390
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18084. .18129
/rpt_Eamily="(TCTA)n"
1869T. .18712
/rpt_Eamily="AT_rich"
19094. .19636
/note="match to EST AL037616 (NID:g5928217)"
19686. .19709
/rpt_Eamily="AT_rich"
19804. .19825
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Maximum Match 100%
Listing first 45 summaries
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Maximum DB seq length: 2000000000
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Perfect score:
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                                                                                                                                                                                                           Score
      N_Geneseq_101002:*

1: /SIDS2/gcgdata/geneseq/geneseqn-embl/NA1980.DAT:*

2: /SIDS2/gcgdata/geneseq/geneseqn-embl/NA1981.DAT:*

3: /SIDS2/gcgdata/geneseq/geneseqn-embl/NA1982.DAT:*

4: /SIDS2/gcgdata/geneseq/geneseqn-embl/NA1983.DAT:*

5: /SIDS2/gcgdata/geneseq/geneseqn-embl/NA1984.DAT:*

6: /SIDS2/gcgdata/geneseq/geneseqn-embl/NA1985.DAT:*

7: /SIDS2/gcgdata/geneseq/geneseqn-embl/NA1987.DAT:*

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9: /SIDS2/gcgdata/geneseq/geneseqn-embl/NA1987.DAT:*

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Gapop 10.0 , Gapext 1.0
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/SIDS2/gcgdata/geneseq/geneseqn-emb1/NA1993.DAT:*
/SIDS2/gcgdata/geneseq/geneseqn-emb1/NA1994.DAT:*
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/SIDS2/gcgdata/geneseq/geneseqn-emb1/NA2001B.DAT:*
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Copyright (c) 1993 - 2003 Compugen Ltd.
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  AAT88851
ABL15860
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ABL32078
AAD28368
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AAK84300
AAK84301
ABL34024
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                                                                                   Drosophila melanog
Drosophila melanog
Human immune syste
Human chemically t
                                                                                                                                                                                                         Description
                       Human
                                          Human immune/haema
                                                                Human
                                                                                                                                                                 cDNA for Macadamia
immune/haema immune syste
                                                              immune/haema
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an	91	24	11046	6.5		45
anscript	ABK28346	2	8440		N	
ylococcu	47	24	1422		Ν	43
Human polynucleoti	AAI83912	22	397		32.2	42
Human DNA differen	ABK83568	24	201143		2	41
cDNA encoding Plas	AAT41852	17	9789	•	2	40
genome	ABS08145	24	463		2	39
usec	AAI39099	22	463		'n	38
	Δ	22	463		32.4	37
3	AAK33310	22	463			36
Human brain expres	AAK07518	22	463	•	2	35
Probe #6488 for ge	ABA28022	22	463		2	34
Human foetal liver	ABA59299	22	463		'n	ü
DNA transcription	ABK28430	24	17142			32
Human immune syste	ABL34107	24	17142		2	31
Chemically pretrea	AAS45498	22	17142			30
cally	AAD28377	24	6041			29
a	ABK40061	24	13784			28
Arabidopsis thalia	AAC48974	21	11220		2	27
	ABL32737	24	5497	6.7		26
Human polynucleoti	AAI84087	22	402			25
r	AAF28545	22	62909	6.7	ω ω	24
Human nervous syst	ABA15292	22	8846	6.7	S S	23
Human cDNA differe	ABK84795	24	139389	٠	33.2	22
Drosophila melanog	ABL30286	23	4936		33.2	21
Pneumococcal patho	ABK83161	24	- 1		33.4	20
Human immune/haema	AAK79382	22	25577		33.4	19
	2	22	10	٠	33.4	18
Streptococcus pneu	AAV52192	19	9223		33.4	17
	w	24	777		33.4	16
sophila mela	ABL03306	23	7978		34	15
	J	20	374	7.0	4.	14
dysferlin	287	21	179	7.1	4	13
dysferlin	67	21	179	7.1	4.	12
transduct	315	24	4	7.1	35.2	11
Tumour suppressor	AAS46745	22		7.1		10

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ALIGNMENTS

RESULT 1 AAT88851

AAT88851;

27-MAR-1998 (first entry)

AAT88851 standard; cDNA; 480

ВP

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mat_peptide cDNA for Macadamia integrifolia antimicrobial protein 1. sig_peptide 31-JAN-1996; 31-JAN-1997; 07-AUG-1997. WO9728185-A1. Macadamia integrifolia. Antimicrobial protein 1; growth inhibition; fungus; bacterium; fungi; bacteria; pathogen control; ss. 96AU-0007802 97WO-AU00052. /*tag= b 148..375 /*tag= c /*tag= a 70..147 /product= antimicrobial_protein_1 Location/Qualifiers

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23-MAR-2000; 2000US-191637P.
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                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                       1 ATTAAGTCTTTGAGTCTCATACATACTCTTCTCCTCCCCACCATTAGCACTTATCAGCTA 60
                                                                                                                                                                                                                          1 ATTAAGTCTTTGAGTCTCATACATACTCTTCTCCTCCCCCACCATTAGCACTTATCAGCTA 60
                                                                                                               The present sequence encodes Macadamia integrifolia antimicrobial protein 1, which exerts inhibitory activity on the growth of fungiand bacteria. It can be used for the control of pathogens in plants
                                                                New anti-microbial protein from Macadamia integrifolia - active in inhibiting the growth of fungi and bacteria in plants and animals
                                                                                                                                                                                                                                                                           ACCTCAGCCATGGCTTCCACCAAGTTGTTCTTCTCAGTCATTACTGTGATGATGCTCATA
                                                                                                                                                                                                                                                                                                                 121 GCAATGGCAAGTGAGATGGTGAATGGGAGTGCATTTACAGTATGGAGTGGTCCAGGTTGT
                                                                                                                                                                                                                                                                                                                                            181 AACAACCGTGCTGAGCGATATAGCAAGTGTGGATGCTCAGCTATACATCAGAAGGGAGGC
                                                                                                                                                                                                                                                                                                                                                          AACAACCGTGCTGAGCGATATAGCAAGTGTGGATGCTCAGCTATACATCATCAGAAGGGAGGC
                                                                                                                                                                                                                                                                                                                                                                                  TATGACTTCAGCTACACTGGACAAACTGCTGCTCTCTACAACCAGGCTGGATGCAGTGGT
                                                                                                                                                                                                                                                                                                                                                                                              241 TATGACTTCAGCTACACTGGACAAACTGCTGCTCTCTACAACCAGGCTGGATGCAGGT
                                                                                                                                                                                                                                                                                                                                                                                                                                         361 ATCTTCATCCAATGCTAGATTTCATAACTCTTGGATCCATCTTCTATGTTTTTCAAGTGT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Drosophila; developmental biology; cell signalling; insecticide;
                                                                                                                                                                                                       ö
                    Marcus JP;
                                                                                                                                                                                    Length 480;
                                                                                                                                                                                                      0; Indels
                                                                                                                                                                  Sequence 480 BP; 129 A; 103 C; 108 G; 140 T; 0 other;
                   Harrison SJ, Manners JM,
                                                                                                                                                                                   97.4%; Score 480; DB 18; I
100.0%; Pred. No. 1.1e-142;
tive 0; Mismatches 0;
(RETR-) COOP RES CENT TROPICAL PLANT PATHOLOGY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Claim 2; Page 24; 38pp; English
                                                                                                                                                                                                        Conservative
                   Green JL,
                                     1997-448317/41.
                                                                                                                                                                                   Query Match
Best Local Similarity
                                              P-PSDB; AAW31738
                    Goulter KC,
                                                                                                                                                animals.
                                                                                                                                                                                                       Matches 480;
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The invention relates to an isolated nucleic acid detection reagent capable of detecting 1000 or more genes from Drosophila. The invention is useful in developmental biology and in elucidating cell signalling and cell-cell interactions in higher eukaryotes for the development of insecticides, therapeutics and pharmaceutical drugs. The invention discloses genomic DNA sequences (ABL16176-ABL30511), expressed DNA sequences (ABL16176) and the encoded proteins
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                     New isolated nucleic acid detection reagent for detecting 1000 or more genes from Drosophila and for elucidating cell signalling and cell-cell interactions -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2189 rigogradaracaacrocorricadaracraarararaacrirriraaaaacarararring 2130
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Claim 1; SEQ ID NO 42062; 21pp + Sequence Listing; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 4667 BP; 1342 A; 1037 C; 954 G; 1334 T; 0 other;
                                                                                                                                                                                                                                                                                  Myers EW;
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ID ABL15858 standard; cDNA; 5823
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                                                          23-MAR-2001; 2001WO-US09231.
                                                                                                                     23-MAR-2000; 2000US-191637P.
11-JUL-2000; 2000US-0614150
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pharmaceutical; gene; ss
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                                                                                                                                                                                                                                                                                  Venter JC, Adams M,
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                                                                                                                                                                                                                                                                                                                                             WPI; 2001-656860/75.
P-PSDB; ABB71757.
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27-SEP-2001
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11-JUL-2000; 2000US-0614150

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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       The invention relates to an isolated nucleic acid detection reagent
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                                                                                                                                                                                                  Human; immune system disease; cytosine methylation; antiasthmatic; antiatteriosclerotic; antiantemic; cytostatic; nootropic; neuroprotective; anti-HIV; anticonvulsant; ophthalmological; antirheumatic; antiarthritic; antidiabetic; antipsoriatic;
                                                                                                                                                                      antiinflammatory; cancer; eye disease; arteriosclerosis; anaemia;
acute myeloid leukaemia; Alzheimer's disease; AIDS; epilepsy;
                                                                                                                                                                                                                                                                                Human immune system associated gene SEQ ID NO:
                                                                                                                                                                                                                                                                                                               26-MAR-2002 (first entry)
                                                                                                         Homo sapiens.
                                                                                                                                                       neurofibromatosis;
                                                                                                                                                                                                                                                                                                                                                                            ABL32078 standard;
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              02-JUL-2001; 2001WO-EP07537
                                              03-JAN-2002.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                          GTATTTTATGGAATATATTTAA 3203
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GTATCACCATGTGATGATTTTYA 490
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TGCGTAGAATACAACTCCGTTCAGATACTAAATATAATAACTTTTAAAAACATATATTTG 3286
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GTTTTTCAAGTGTATAATTAGAGAGATGCATGGATATATAATAATAAGTAAAAGCTACG 467
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76; Conserv
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53.1%;
                                                                                                                                                                                                                                                                                                                                                                              DNA;
                                                                                                                                                         rheumatoid arthritis; psoriasis;
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RESULT 5
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Best Local 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       The present invention provides a number of human immune system associated genes which are modified by the methylation of cytosines. The sequences can be used in the diagnosis and treatment of immune system disorders, including eye diseases such as retinopathy, neovascular glaucoma and macular degeneration, arteriosclerosis, anaemia, cancer, acute myeloid leukaemia, Alzheimer's disease, ADDS, eppliepsy, neurofibromatosis, rheumatoid arthritis, psoriasis and inflammatory/ulcerative bowel diseases. The present sequence is a gene of the invention.
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01-SEP-2000; 2000DE-1043826.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Nucleic acid comprising fragment of chemically modified for diagnosis and treatment of diseases associated with
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WPI; 2002-130909/17.
                                                                                                                                                                                                                                                                                       Human; cytostatic; antidepressant; neuroleptic; nootropic; antiaddictive; adrenergic alpha-1C-receptor; cytosine methylation; therapy; alcoholism; behavioural disorder; neurological; psychiatric; cancer; schizophrenia; Tourette's syndrome; smoking; human immunodeficiency virus dementia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   cytosine methylation
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                                                                                                                 30-JUN-2000; 2000DE-1032529
01-SEP-2000; 2000DE-1043826
                                                                                                                                                                                                                                                                                                                                                                     Human chemically treated genomic DNA #9.
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                                                                                                                                                           02-JUL-2001; 2001WO-EP07540
                                                                                                                                                                                          10-JAN-2002
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                                                                                                                                                                                                                                                  Homo sapiens.
                           WPI; 2002-154759/20.
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                                                                                                                                                                                                                                                                              abuse; migraine;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ATCTAAATTTAACCCAAATCTACCTAAATCCAAAACCCATCTTTAATCTTTCAATATA 3088
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     7.2%;
Similarity 58.5%;
                                                                                     EPIGENOMICS AG
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                                                       Piepenbrock
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Novel nucleic acid useful

for diagnosis and therapy

of behavioral

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The invention relates to nucleic acids comprising a segment of chemically pretreated DNA of adrenergic alpha-1C-receptor gene. The invention also betalates to oligonuclectides or peptide nucleic acid (PNA) oligomers useful for detecting cytosine methylations. The pretreated DNA is useful for the diagnosis or therapy of behavioural disorders, neurological disorders and cancer, in particular major depressive disorder, Tourette's syndrome, schizophrenia, psychiatric and neurological disorders, smoking, drug abuse, alcoholism, personality traits, compulsive gambling, human and schizoaffective patients, and sucidal behaviours in schizophrenic and schizophrenia. The nucleic acid is useful for detecting the methylation state of all CpG dinucleotides and/or single nucleotide polymorphisms (SNPS). The present sequence is human chemically treated genomic DNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         3147 Archaartraacccaaarcraacraaarccaaaacccarcrirraarcrarara 3088
disorder, neurological disorder and cancer, comprises a sequence of a segment of chemically pretreated DNA of adrenergic alpha-1C-receptor gene -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       361 ATCTTCATCCAATGCTAGATTTCATAACTCTTGGATCCATCTTCTATGTTTTTCAAGTGT 420
                                                                                                                                                                                                                                                                                                                                                                                                Query Match 7.2%; Score 35.6; DB 24; Length 8011;
Best Local Similarity 58.5%; Pred. No. 2.3;
Matches 62; Conservative 0; Mismatches 44; Indels 0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Human immune/haematopoietic antigen genomic sequence SEQ ID NO:39114.
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                                                                                                                                                                                                                                                                                                                                                                Sequence 8011 BP; 1986 A; 145 C; 1776 G; 4104 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           421 ATAATTAGAGAGATGCATGGATATATAATAAATAAGTAAAAGCTAC 466
                                                                         Claim 1; Page 56-60; 190pp; English.
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16-MAR-2000; 2000US-0189874.

17-MAR-2000; 2000US-0190076.

18-APR-2000; 2000US-019123.

19-MAY-2000; 2000US-0209467.

28-JUN-2000; 2000US-0219467.

28-JUN-2000; 2000US-0214886.

30-JUN-2000; 2000US-0214886.
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2000US-0217496.
2000US-0218290.
2000US-0220963.
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2000US-0184664.
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14-JUL-2000;
26-JUL-2000;
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24-FEB-2000;
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2000US-0225213.
2000US-0225214.
2000US-022526.
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2000US-0225270.
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2000US-0225758.
2000US-0225759,
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2000US-0229509.
2000US-0229513.
2000US-0230437.
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2000US-0231242.
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2000US-0232397.
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2000US-0232400.
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2000US-0233063.
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2000US-0234274.
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2000US-0236367.
2000US-0236368.
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14-AUG-2000;
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22-AUG-2000;
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AAK54951 to AAK64702 encode the human immune/haematopoietic antigen (I) amino acid sequences given in AAM82170 to AAM91921. (I) have cytostatic activity, and can be used in gene therapy and vaccine production. (I) proteins and polynucleotides may be used in the prevention, diagnosis and treatment of diseases associated with inappropriate (I) expression. For certain the precipitying mutations or deletions in a patient's genome cappelement the patients own production of (I). Additionally, (I) polynucleotides may be used to produce the secreted (I), by inserting the nucleotides may be used to produce the secreted (I), by inserting the nucleic acids into a host cell and culturing the cell to express the protein. (I) proteins and polynucleotides may be used to produce the secreted to prevent.

CC diagnose and treat immune/haematopoietic-related diseases, especially cancers and cancer metastases of haematopoietic-derived cells. AAK64703
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08-NOV-2000;
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17-NOV-2000;
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08-NOV-2000;
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06-DEC-2000;
08-DEC-2000;
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08-DEC-2000;
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                                                                                                                                                                                                                          NUCLEIC acids encoding human immune/hematopoietic antigen polypeptides, useful for preventing, diagnosing and/or treating cancers and metastasis -
                                                                                                                                                                                             Disclosure; SEQ ID NO 39114; 3071pp + Sequence Listing; English.
                                                                                                                                                                                                                                                                           WPI; 2001-483426/52.
                                                                                                                                                                                                                                                                                                                              (HUMA-) HUMAN GENOME SCI INC
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2000US-0246477.
2000US-0246478.
2000US-0246523.
2000US-0246523.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      to AAK87694 represent human immune/haematopoietic antigen genomic sequences from the present invention. AAK54942 to AAK54950 and AAM82169 represent sequences used in the exemplification of the present invention.
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                                                                                                             11-JUL-2000;
14-JUL-2000;
26-JUL-2000;
26-JUL-2000;
                                                                                                                                                                  30-JUN-2000;
07-JUL-2000;
07-JUL-2000;
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14-AUG-2000;
14-AUG-2000;
14-AUG-2000;
14-AUG-2000;
14-AUG-2000;
14-AUG-2000;
14-AUG-2000;
14-AUG-2000;
14-AUG-2000;
                                                                                                                                                                                                                                                                                                                                                                                               Human; immune; haematopoietic; immune/haematopoietic antigen; cancer; cytostatic; gene therapy; vaccine; metastasis; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                               Human immune/haematopoietic antigen genomic sequence SEQ ID NO:39112
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                                                                                                                                                                                                                                                                                                                                                                               Homo sapiens.
                                                                                                                                                                                                                                                                                                                 17-JAN-2001; 2001WO-US01354
                                                                                                                                                                                                                                                                                                                                                           WO200157182-A2
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28-JUN-2000;
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18-APR-2000;
                                                                                                                                                        11-JUL-2000;
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         2000US-0224519.
2000US-0225214.
2000US-0225214.
2000US-0225266.
2000US-0225267.
2000US-0225268.
2000US-02252768.
2000US-0225276.
2000US-0225447.
2000US-0225757.
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2000US-0224518.
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2000US-0218290.
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2000US-0217487.
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Pred. No. 2
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0; Mismatches
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2000US-0231414.
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08-NOV-2000; 2000US-0246478
08-NOV-2000; 2000US-0246523
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08-NOV-2000; 2000US-0246524.
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22-AUG-2000;
22-AUG-2000;
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06-SEP-2000
06-SEP-2000
08-SEP-2000
08-SEP-2000
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08-NOV-2000;
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2000US-0249211
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2000US-0249216
2000US-0249216
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    08-NOV-2000;
17-NOV-2000;
17-NOV-2000;
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17-NOV-2000;
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17-NOV-2000;
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(HUMA-) HUMAN GENOME SCI INC

Rosen CA, Barash SC, Ruben SM;

WPI; 2001-483426/52.

Nucleic acids encoding human immune/hematopoietic antigen polypeptides, useful for preventing, diagnosing and/or treating cancers and metastasis -

Disclosure; SEQ ID NO 39112; 3071pp + Sequence Listing; English.

AAK54951 to AAK64702 encode the human immune/haematopoietic antigen (I)

amino acid sequences given in AAM8210 to AAM91921. (I) have cytostatic
acituity, and can be used in gene therapy and vaccine production. (I)
acituity, and can be used in gene therapy and vaccine production. (I)
treatment of diseases associated with inappropriate (I) expression. For
example, they may be used to treat disorders associated with decreased
cytostation by rectifying mutations or deletions in a patient's genome
that affect the activity of (I) by expressing inactive proteins or to
cyplomucleotides may be used to production of (I). Additionally, (I)
cyplomicleotides may be used to produce the secreted (I), by inserting
the nucleic acids into a host cell and culturing the cell to express the
cyclein. (I) proteins and polynucleotides may be used to prevent,
diagnose and treat immune/haematopoietic-related diseases, especially
cancers and cancer metastases of haematopoietic derived cells. AAK64703
cyclein. (I) proteins and polynucleotides may be used to prevent,
cancers and cancer metastases of haematopoietic antigen genomic
cyclein. (I) proteins and polynucleotides may be used to prevent,
cancers and cancer metastases of haematopoietic antigen genomic
cyclein. (I) expressent invention. AAK54950 and AAM82169
cyclein. (I) expressent invention. AAK54950 and AAM82169
cyclein. (I) expressent invention.

Sequence 8209 BP; 2721 A; 1260 C; 1380 G; 2848 T; 0 other;

0; Gaps Query Match
7.2%; Score 35.4; DB 22; Length 9209;
Best Local Similarity 55.2%; Pred. No. 2.7;
Matches 69; Conservative 0; Mismatches 56; Indels 0;

345 TITIGGINGGAAGAGTATCTICATCCAATGCTAGATTTCATAACTCTTGGATCCATCTTC 404

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RESULT 8
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        14-JUL-2000
26-JUL-2000
14-AUG-2000
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23-AUG-2000
01-SEP-2000
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01-SEP-2000
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20-OCT-2000

20-OCT-2000

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2000US-0241809.

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2000US-0235834
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AAKS4951 to AAK64702 encode the human immune/haematopoietic antigen (I)

amino acid sequences given in AAM82170 to AAM91921. (I) have cytostatic
activity, and can be used in gene therapy and vaccine production. (I)
proteins and polynucleotides may be used in the prevention, diagnosis and
creample, they may be used to treat disorders associated with decreased
c example, they may be used to treat disorders associated with decreased
cc expression by rectifying mutations or deletions in a patient's genome
that affect the activity of (I) by expressing inactive proteins or to
c supplement the patients own production of (I). Additionally, (I)
c supplement the patients own production of (I). Additionally, (I)
c polynucleotides may be used to produce the secreted (I), by inserting
cc the nucleic acids into a host cell and culturing the cell to express the
creancers and cancer metastases of haematopoietic-derived cells. AAK64703
cc cancers and cancer metastases of haematopoietic-derived cells. AAK64703
cc cancers and cancer metastases of haematopoietic antigen genomic
c to AAK87694 represent human immune/haematopoietic antigen genomic
c represent sequences used in the exemplification of the present invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Nucleic acids encoding human immune/hematopoietic antigen polypeptides, useful for preventing, diagnosing and/or treating cancers and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2563 TATTTGTAGGAATGCCAACTCATTTTAAATTTTTTTTGCATTTGCAACATTTTTC 2622
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Best Local Similarity 55.2%; Pred. No. 2.7;
Matches 69; Conservative 0; Mismatches 56; Indels 0;
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                                                          2000US-0249244.
2000US-0249245.
2000US-0249264.
2000US-0249265.
2000US-0249265.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WPI; 2001-483426/52
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                                                                                                                                                                                                                                                                                                                                                                                                                05-DEC-2000; 205-DEC-2000; 206-DEC-2000; 206-DEC-2000; 206-DEC-2000; 206-DEC-2000; 206-DEC-2000; 206-DEC-2000; 206-DEC-2000; 206-DEC-2000; 206-DEC-2000; 206-DEC-2000; 206-DEC-2000; 206-DEC-2000; 206-DEC-2000; 206-DEC-2000; 206-DEC-2000; 206-DEC-2000; 206-DEC-2000; 206-DEC-2000; 206-DEC-2000; 206-DEC-2000; 206-DEC-2000; 206-DEC-2000; 206-DEC-2000; 206-DEC-2000; 206-DEC-2000; 206-DEC-2000; 206-DEC-2000; 206-DEC-2000; 206-DEC-2000; 206-DEC-2000; 206-DEC-2000; 206-DEC-2000; 206-DEC-2000; 206-DEC-2000; 206-DEC-2000; 206-DEC-2000; 206-DEC-2000; 206-DEC-2000; 206-DEC-2000; 206-DEC-2000; 206-DEC-2000; 206-DEC-2000; 206-DEC-2000; 206-DEC-2000; 206-DEC-2000; 206-DEC-2000; 206-DEC-2000; 206-DEC-2000; 206-DEC-2000; 206-DEC-2000; 206-DEC-2000; 206-DEC-2000; 206-DEC-2000; 206-DEC-2000; 206-DEC-2000; 206-DEC-2000; 206-DEC-2000; 206-DEC-2000; 206-DEC-2000; 206-DEC-2000; 206-DEC-2000; 206-DEC-2000; 206-DEC-2000; 206-DEC-2000; 206-DEC-2000; 206-DEC-2000; 206-DEC-2000; 206-DEC-2000; 206-DEC-2000; 206-DEC-2000; 206-DEC-2000; 206-DEC-2000; 206-DEC-2000; 206-DEC-2000; 206-DEC-2000; 206-DEC-2000; 206-DEC-2000; 206-DEC-2000; 206-DEC-2000; 206-DEC-2000; 206-DEC-2000; 206-DEC-2000; 206-DEC-2000; 206-DEC-2000; 206-DEC-2000; 206-DEC-2000; 206-DEC-2000; 206-DEC-2000; 206-DEC-2000; 206-DEC-2000; 206-DEC-2000; 206-DEC-2000; 206-DEC-2000; 206-DEC-2000; 206-DEC-2000; 206-DEC-2000; 206-DEC-2000; 206-DEC-2000; 206-DEC-2000; 206-DEC-2000; 206-DEC-2000; 206-DEC-2000; 206-DEC-2000; 206-DEC-2000; 206-DEC-2000; 206-DEC-2000; 206-DEC-2000; 206-DEC-2000; 206-DEC-2000; 206-DEC-2000; 206-DEC-2000; 206-DEC-2000; 206-DEC-2000; 206-DEC-2000; 206-DEC-2000; 206-DEC-2000; 206-DEC-2000; 206-DEC-2000; 206-DEC-2000; 206-DEC-2000; 206-DEC-2000; 206-DEC-2000; 206-DEC-2000; 206-DEC-2000; 206-DEC-2000; 206-DEC-20000; 206-DEC-2000; 206-DEC-2000; 206-DEC-2000; 206-DEC-2000; 206-DEC-2000; 206-DEC-2000; 206-DEC-2000; 206-DEC-2000; 206-DEC-2000; 206-DEC-2000; 206-DEC-2000; 206-DEC-2000; 206-DEC-2000; 206-DEC-2000; 206-DEC-2000; 206-DEC-2000; 206-DEC-2000; 206-DEC-2000; 20
                                                                                                                                      17-NOV-2000;
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셤
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The present invention provides a number of human immune system associated genes which are modified by the methylation of cytosines. The sequences can be used in the diagnosis and treatment of immune system disorders, including eye diseases such as retinopathy, neovascular glaucoma and macular degeneration, arteriosclerosis, anaemia, cancer, acute myeloid leukeamia, Alzheimer's disease, Alls, epilepsy, neurofibromatosis, rheumatoid arthritis, psoriasis and inflammatory/ulcerative bowel diseases. The present sequence is a gene of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2241 iririridrakdariaririrraarrakidecederirirarrakrirarrakrakraka 2300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              346 TITGGITGGAAGAGIATCITCATCCAATGCTAGATTTCATAACTCTTGGATCCATCTTCT 405
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0; Сарв
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Nucleic acid comprising fragment of chemically modified gene, useful for diagnosis and treatment of diseases associated with abnormal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       antiarteriosclerotic; antianaemic; cytostatic; nootropic; neuroprotective; anti-HIV; anticonvulsant; ophthalmological; antirheumatic; antiarthritic; antidiabetic; antipsoriatic; antiinflammatory; cancer; eye disease; arteriosclerosis; anaemia; acute myeloid leukaemia; Alzheimer's disease; AIDS; epilepsy; neurofibromatosis; rheumatoid arthritis; psoriasis; bowel disease;
                                                                                                                                                          Human; immune system disease; cytosine methylation; antiasthmatic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
7.1%; Score 35.2; DB 24; Length 6375;
Best Local Similarity 55.8%; Pred. No. 2.7;
Matches 67; Conservative 0; Mismatches 53; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 6375 BP; 1795 A; 207 C; 1431 G; 2942 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Claim 1; SEQ ID NO 1997; 32pp + Sequence Listing; German.
                                                                                                                       Human immune system associated gene SEQ ID NO: 1997.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Berlin K;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAS46745 standard; DNA; 38342 BP
           ABL34024 standard; DNA; 6375 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                           02-JUL-2001; 2001WO-EP07537.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            30-JUN-2000; 2000DE-1032529.
01-SEP-2000; 2000DE-1043826.
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                                                                                      (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EPIG-) EPIGENOMICS AG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                cytosine methylation
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                                                                                                                                                                                                                                                                                                                                                                  WO200200928-A2.
                                                                                                                                                                                                                                                                                                                                 Homo sapiens.
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                                                                                      26-MAR-2002
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ABL34024
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2683 ÁCTGT 2687

derived chemically modified sequence #469.

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RESULT 11
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Best Local :
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                                          Sequence 38342 BP; 11153 A; 472 C; 7565 G; 19152 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The invention relates to a nucleic acid comprising a sequence of 18 bases, of a segment of chemically pretreated DNA (CP DNA) e.g. with bisulphite, of genes associated with tumour suppression and oncogenes having a sequence taken from 536 (actually 53 since numbers 408, 458 and 500 are missing from the sequence listing) sequences, and sequences complementary to (Ss). The nucleic acid may be a peptide nucleic acid-oligomer (PNA) of at least 9 nucleotides and may form the sequences.
                                                                                                                                                                                                                                                                                                                Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   15-MAR-2000;
06-APR-2000;
07-APR-2000;
30-JUN-2000;
                                                                                     406
                                                                                                                                                                                                                                                                                          ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Claim 1; SEQ ID No 469; 27pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Fragments of chemically modified genes associated with tumour suppressor genes and oncogenes, useful in designing primers and probes for analysing diseases associated with cytosine methylation state e.g.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WPI; 2001-602752/68
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                07-APR-2000; 2000DE-1019173.
30-JUN-2000; 2000DE-1032529.
01-SEP-2000; 2000DE-1043826.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Human; tumour suppressor gene; oncogene; antitumour; cytostatic; cancer; tumour; CpG dinucleotide; single-nucleotide polymorphism; SNP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         15-MAR-2001; 2001WO-EP02955.
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                                                                                                                                                                                                         Local
                                                                                                                                                                                                                                                                                                                                                                                genomic sequences derived from tumour suppressor genes
                                                                          TITGGTTGGAAGAGTATCTTCATCCAATGCTAGATTTCATAACTCTTGGATCCATCTTCT 405
                                                                                                                                                                                          67;
                                                                                                                                                                                                           Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EPIGENOMICS AG
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                                                                                                                                                                                          Conservative
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                                                                                                                                                                                                       Score 35.2; DB 22; Pred. No. 6.8;
                                                                                                                                                                                        Mismatches
                                                                                                                                                                                       53;
                                                                                                                                                                                       Indels
                                                                                                                                                                                                                      Length 38342;
                                                                                                                                                                                   0; Gaps
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                                                                                                                                                                                                                                     CC signal transduction associated genes. The DNA sequences are chemically CC modified using a solution of bisulphite, hydrogen sulphite or disulphite. Also disclosed are oligonucleotides and/or PNA oligoners CC for detecting the cytosine methylation state (CpG islands) of these CC genes, and a method for the diagnosis and/or therapy of genetic and CC gengenchic parameters of genes associated with signal transduction. CC contain DNA, e.g. cell lines, biopsies, blood, sputum, stool, urine, CC cortain DNA, e.g. cell lines, biopsies, blood, sputum, stool, urine, CC crebral-spinal fluid, tissue embedded in paratfin such as tissue from CC eyes, intestine, kidney, brain, heart, prostate, lung, breast or liver, CC histologic object slides, and all their possible combinations. The CC diseases associated with signal transduction e.g. solid tumours and CC sequences of the invention are useful for the diagnosis and therapy of classases associated with signal transduction e.g. solid tumours and CC sequences of different genes associated with signal transduction, or their complementary camesons associated with signal transduction, or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ABK31506
                                                                                                                                                                              Query Match
Best Local
                                                                                                                                                                                                                           Sequence 38342 BP; 11153 A; 472 C; 7565 G; 19152 T; 0 other;
                                                                                                                                                                                                                                                                                their complementary sequences.

Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Oligonuclectide for diagnosis and therapy of diseases associated with signal transduction e.g. cancer, comprises chemically modified genomic
                                                                                                          346 TTTGGTTGGAAGAGTATCTTCATCCAATGCTAGATTTCATAACTCTTGGATCCATCTTCT 405
                                                                                                                                                                                                                                                                         European Patent Office
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The present invention relates to chemically modified DNA sequences of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Claim 1; SEQ ID No 349; 24pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      sequences of genes associated with signal transduction
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WPI; 2002-147896/19.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Olek A,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  30-JUN-2000; 2000DE-1032529; 01-SEP-2000; 2000DE-1043826;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Human; signal transduction associated gene; cytosine methylation state; CpG island; signal transduction associated disease; solid tumour; cancer; antitumour; cytostatic; mutant; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           29-JUN-2001; 2001WO-EP07472
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Synthetic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Signal transduction associated gene modified DNA #175
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ABK31506 standard; DNA; 38342
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            23-APR-2002 (first entry)
                                                                                                                                                                            Local Similarity
                                 67;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Piepenbrock C,
                                                                                                                                                          Conservative
                                                                                                                                                                          7.1%;
55.8%;
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                                                                                                                                                        0
                                                                                                                                                      Score 35.2; DB 24;
Pred. No. 6.8;
0; Mismatches 53;
                                                                                                                                                                                         Length 38342;
                                                                                                                                                      Indels
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                                                                                                                                                  Gaps
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The present invention describes an isolated dysferlin DNA of 20-25

uncleotides in length, comprising a nucleotide sequence specifically
selected from nucleotides 911-913, 929-948, 1019-1038, 1392-1411,
1424-1443, 1484-1503, 1499-1518, 11543-1565, 1715-1734, 1714-1759,
1724-1443, 1484-1503, 1499-1518, 1543-1565, 1715-1734, 1714-1759,
1724-1443, 1484-1503, 1499-1518, 1543-1565, 1716-1734, 1714-1759,
1724-1443, 1484-1503, 1499-1518, 1563-16694,
1724-1443, 1484-1503, 1499-1518, 1563-16694,
1724-1443, 1484-1503, 1499-1518, 1563-16694,
1724-1443, 1484-1503, 1499-1518, 1563-16694,
1724-1443, 1484-1503, 1499-1518, 1563-16694,
1724-1443, 1484-1503, 1499-1518, 1563-16694,
1724-1443, 1484-1503, 1499-1518, 1653-16694,
1724-1443, 1484-1503, 1499-1518, 1699-1696,
1724-1443, 1484-1503, 1499-1518, 1699-1696,
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1724-1443, 1484-1696
                                                                                                                                                                                                                                         Human; dysferlin; mutant; identification; chromosome 2p12-14; detection; muscular dystrophy; diagnosis; hereditary muscular dystrophy; miyoshi myopathy; limb girdle muscular dystrophy; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Dysferlin polynucleotide, its mutant form useful for diagnosis and treatment of hereditary muscular dystrophies e.g. miyoshi myopathy and limb girdle muscular dystrophy -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          7.1%; Score 34.8; DB 21; Length 179; 65.4%; Pred. No. 0.6; tive 0; Mismatches 27; Indels 0;
                                                                                                                                                                                            Human dysferlin related nucleotide sequence SEQ ID NO:43.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 179 BP; 42 A; 34 C; 66 G; 37 T; 0 other;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Disclosure; Page 101; 136pp; English.
                                             AAA36785 standard; DNA; 179 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Brown RH, Liu J, Hoffman E,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           99WO-US19394.
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                                                                                                                                                  03-AUG-2000 (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                           WO200011016-A1.
                                                                                                                                                                                                                                                                                                                                                            Homo sapiens.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              25-AUG-1998;
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                                                                                                  AAA36785;
RESULT 12
                          AAA36785/
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This invention describes a novel human dysferlin nucleic acid (I) and its encoding protein (II), which has anti-dystrophic activity and can be used for gene therapy. Introduction of (I), a vector comprising (I) or dysferlin into a cell of a mammal can be used to decrease the symptoms of muscular dystrophy. The dysferlin gene is normally expressed in skeletal muscle cells and is selectively mutated in several families with the hereditary muscular dystrophies, e.g. Miyoshi myopathy and limb girdle muscular dystrophies and oligonucleotides derived from (I) can be used in diagnosis of or risk identification for dysferlin-related
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        disorders in patients, fetus, or pre-embryos. Expression of brain-specific dysferlin may be important as a marker for normal neural development. Dysferlin DNA or subgenomic coding sequences can be used for therapy of the hereditary muscular dystrophies. This sequence represents a fragment of the human dysferlin gene described in the method of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Novel dysferlin genes and related proteins useful for diagnosis, risk identification and treatment of hereditary muscular dystrophies and other dysferlin related disorders -
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          22 CATACTCTTCTCCTCCCCACCATTAGCACTTATCAGCTAACCTCAGCCATGGCTTCCACC 81
                                                                                                                                                                                                                                                                  Dysferlin, anti-dystrophic, gene therapy; muscular dystrophy; human; skeletal muscle cell; hereditary; Miyoshi myopathy; diagnosis; limb girdle muscular dystrophy-2B; brain-specific; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              7.1%; Score 34.8; DB 21; Length 179; larity 65.4%; Pred. No. 0.6; Conservative 0; Mismatches 27; Indels 0.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 179 BP; 42 A; 34 C; 66 G; 37 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Brown RH, Liu J, Aoki M, Ho MF, Matsuda-Asada C;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Claim 11; Page 111; 146pp; English.
                                                                                                                  ВР
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    98US-0097927.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                99WO-US19395.
                                                                                                                  AAX82876 standard; DNA; 179
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            95 AAGTICTICTIGITACTC 78
95 AAGTTCTTCTTGTTACTC 78
                                                                                                                                                                                            (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (GEHO ) GEN HOSPITAL CORP.
                                                                                                                                                                                                                                  Human dysferlin DNA #24.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WPI; 2000-237646/20.
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nes 51; Conserv
                                                                                                                                                                                                                                                                                                                                                                                      WO200011157-A1.
                                                                                                                                                                                                                                                                                                                                                    Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                25-AUG-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      25-AUG-1998;
                                                                                                                                                                                              30-JUN-2000
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RESULT 14 AAV87102

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22 CATACTCTTCTCCTCCCCACCATTAGCACTTATCAGCTAACCTCAGCCATGGCTTCCACC 81 155 cerecricerrectracearitricececaaadereactecacaaadesececae

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82 AAGTTGTTCTTCAGTC 99

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Best Local Similarity
Matches 85; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    and thrombolytic activity, receptor/ligand activity, anti-inflammatory activity, cadherin/tumour invasion suppressor activity, tumour inhibition activity. The EST sequences are also stated to be useful for gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            New polynucleotides encoding human secreted proteins - derived e.g. human blood, kidney, foetal lung, placenta, testes, brain, ovary, pituitary, retina and colon cDNA libraries
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Expressed sequence tag; secreted protein; haematopoiesis regulator; tissue growth; activin; inhibin; tumour invasion suppressor; EST; human; chemotaxis; chemokinesis; haemostasis; gene therapy; thrombolysis; receptor; ligand; anti-inflammatory; tumour inhibitor; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 374 BP; 132 A; 69 C; 48 G; 125 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Claim 1; Page 453; 633pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             10-APR-1998;
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                                                                                                                                                                                                                                                                                      400
                                                                                                                                                                                                                                                                                                                                         211
                                                                                                                                                                                                                                                                                                                                                                            340 AACCCTTTTGGTTGGAAGAGTATCTTCATCCAATGCTAGATTTCATAACTCTTGGATCCA 399
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                                                                                                                                                            AAGCTACGGTATCACCATGTGATGATTTTYACCC
                                                                                                                                                                                                                                                                        AATGCTTTTTAAAGGAAAAAAACATGAAATCAAATAATAGATTT-TCACTTAATTCAATTT 269
                                                                                                                            GAAGTACAGAATTCCCATATAATCACTTTTCCCC
                                                                                                                                                                                                                                TTTGTTTTGTTTTAATTTTCAATTACTAGACAGATCTAGGTTTATAAAAGAACTAAACAG
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55.2%;
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Treacy M;
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                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 34.4; DB Pred. No. 1.2; 1; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                          67;
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ABL03306 standard; cDNA;

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Matches
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                                                                                                                                                                                                                                                                                                                                             The invention relates to an isolated nucleic acid detection reagent capable of detecting 1000 or more genes from Drosophila. The invention useful in developmental biology and in elucidating cell signalling and cell-cell interactions in higher eukaryotes for the development of insecticides, therapeutics and pharmaceutical drugs. The invention discloses genomic DNA sequences (ABL16176-ABL30511), expressed DNA sequences (ABL01840-ABL16175) and the encoded proteins
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Drosophila; development pharmaceutical; gene;
                                                                                                                                                                                                                                                   Sequence 7978 BP; 2487 A; 1370 C; 1394 G; 2727 T; 0 other;
                                                                                                                                                                                                                                                                               The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Claim 1; SEQ ID NO 4400; 21pp + Sequence Listing; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       genes from Drosophila
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WPI; 2001-656860/75.
P-PSDB; ABB59203.
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11-JUL-2000;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         New isolated nucleic acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       26-MAR-2002
                                                                                                                                                                                                                                                                                                                                     (ABB57737-ABB72072)
                                                                                                                                                                                                      Match 6.9%;
Local Similarity 50.6%;
                                                                                                                                                        CCAGGGCATGCAACCCTTTTGGTTGGAAGAGTATCTTCATCCAATGCTAGATTTCATAAC 388
                                TARATAAGTAARAGCTACGGTATCACCATGTGATGATTTTYA 490
                                                                                           TCTTGGATCCATCTTCTATGTTTTTCAAGTGTATAATTAGAGAGATGCATGGATATATAA 448
                                                                                                                           CAAGGGGCACCTCCGCTTTTCGTGGTTATCAATGCCTAAGCCATTGAAATATTATTATTAT 7243
TACAGTCTGAAAATATGCGTTTATACGAGCGGATAATTTTAA 7141
                                                             82;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         developmental biology; cell signalling; insecticide;
cal; gene; ss.
                                                                                                                                                                                          Conservative
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2000US-0614150.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    acid detection reagent for detecting 1000 or more and for elucidating cell signalling and cell-cell
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Pred. No. 7.
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                                                                                                                                                                                                                      DB 23;
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Perfect score:
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Maximum DB seq length: 200000000
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      Score
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re greater than or equal to the score of the result being printed,
is derived by analysis of the total score distribution.
    January 12, 2003, 07:12:54; Search time 49 Seconds (without alignments) 3085.544 Million cell up
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493
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Gapop 10.0 , Gapext 1.0
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1: /cgn2_6/ptodata/1/ina/5B_COMB.seq:*

2: /cgn2_6/ptodata/1/ina/5B_COMB.seq:*

3: /cgn2_6/ptodata/1/ina/6A_COMB.seq:*

4: /cgn2_6/ptodata/1/ina/6B_COMB.seq:*

5: /cgn2_6/ptodata/1/ina/PCTUS_COMB.seq:*

6: /cgn2_6/ptodata/1/ina/backfiles1.seq:*
 6.8 9223
6.5 537
6.5 537
6.4 6354
6.4 6354
6.4 246240
6.4 246240
6.3 1213
6.3 1213
6.2 13715
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 US-08-961-527-59
US-09-134-001C-1936
US-09-134-5-5395
US-09-134-5-642-5
US-09-058-389A-5
US-09-058-394A-21
US-08-724-394A-21
US-08-724-394A-22
US-07-741-453A-57
US-08-121-446-3
US-08-121-446-3
US-09-600-776-9
US-08-973-462-2
US-07-741-150-3
US-09-600-776-9
US-08-973-462-1
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US-08-98-975-1
US-08-98-975-1
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US-08-98-975-1
US-08-98-975-2
US-08-98-627-28
US-08-990-523-28
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US-08-990-020-818-4
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Sequence 59, Appl
Sequence 5, Appli
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Sequence 20, Appli
Sequence 21, Appli
Sequence 27, Appli
Sequence 37, Appli
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TAT	7 h	TELEFAX)RMATION QUENCE (QUENCTH: LENGTH: TYPE: 1 STRANDE! TOPOLOG:	RNEY ME: GIST COMM	PLIC LING ASSI PLIC	OTER DIUM MPUT ERAT FTWAL	DRESPOINTY:	-527- ie 59, NO. 6 IL INF ICANT		22222	22222	2000 2000 2000 2000 2000 2000 2000	'n
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TATCTTCATCCAATGCTAGATTTCATAACTCT 	6. ty 52. ervative) 309-85 Q ID NO: ERISTICS base pai acid acid double ear	ATTORNEY/AGENT INFORMATION: NAME: Brookes, A. Anders REGISTRATION NUMBER: 36,373 REFERENCE/DOCKET NUMBER: PB3 TELECOMMUNICATION INFORMATION: TELEPHONE: (301) 309-8504	WBER: US : 424 N DATA: WBER:	LE FORM: Diskette, : Vectra 486, Vectra 486, IEM: MSDOS CII Text TION DATA:	West Gen Ss:	n US Kuns Str		1037 1037 1070 1484 1484	618 618 973 1037	150 1517 1794 19124 634 5852	4 7 0
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CATAA	Score Pred. 1; Mi		.73 PB340P N:	08/961,5		Science	61527	ALI	00000	88999	US-08- US-08- US-08- US-08- US-09- US-09-) 26
VICIT	No.		Ä	27	h, 1	s,		ALIGNMENTS	358-7 358-7 299-9 684-0	145-8 177-6 240-1 453-9	S94-07072-6 S94-07072-6 -9263-602-6 -926-268-111-8 -328-111-8 -328-164-1	007-7
TAACTCTTGGATCCAT	4; DB 1.2; ches				. 4МБ в	Inc.	pneumonia	NTS	121-1 734-1 567-8 024-5 868-5	368-3 550-119 124-1 943-1	7072-2 502-6 502-6 270-1 326B-13 111-825 106-2	740-4
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LOCATION: 1.537
CTHER INFORMATION: /product= "melon CmEx1"
US-08-845-539-5
                        TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 337 base pairs
TYPE: nucleic acid
STRANDENNESS: single
                                                                                                                                                                                                                                           MOLECULE TYPE: DNA (genomic)
    REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity 52.78
Matches 69; Conservative
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Matches 69; Conservative
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LENGTH: 537
TYPE: DNA
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APPLICANT: Lynn Doucette-Stamm et al
APPLICANT: Lynn Doucette-Stamm et al
APPLICANT: Lynn Doucette-Stamm et al
APPLICANT: Lynn Doucette-Stamm et al
APPLICANT: Lynn Doucette-Stamm et al
APPLICANT: Lynn WICLEIC ACID AND AMINO ACID SEQUENCES RELATING TO STAPHYLOCOCCUS
TITLE DE INVENTION: BPLDERAIDIS FOR DIAGNOSTICS AND THERAPEUTICS
TITLE OF INVENTION: NUMBER: US 09/134,001C
CURRENT FILING DATE: 1994-08-13
PRIOR FILING DATE: 1997-10-8
RIOR FILING DATE: 1997-10-8
RIOR FILING DATE: 1997-10-8
RIOR FILING DATE: 1997-10-14
NUMBER: OF SEQ ID NOS: 5674
LENGTH: 1422
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Patent No. 5259303
GENERAL INFORMATION:
APPLICANT: Bennett, Alan B.
APPLICANT: Rose, Jocelyn K.C.
TITLE OF INVENTION: Expansin Genes to Control Fruit Texture and Softening NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
ADDRESSEE: Two members and Townsend and Crew LLP
STREET: Two Embarcadero Center, Eighth Floor
CITY: San Francisco
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                                          4911 rccantragaaaaragcrrgraarcaraagaaacaggrgrargcaaargaarraaagrcr 4852
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420 TATAATTAGAGAGATGCATGGATATAATAAATAAGTAAAAGCTACGGTATCACCATGT 479
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    371 AATGCTAGATTTCATAACTCTTGGATCCATCTTCTATGTTTTTCAAGTGTATAATTAGAG 430
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match 6.5%; Score 32.2; DB 4; Length 1422; Best Local Similarity 57.4%; Pred. No. 1.1; Matches 58; Conservative 0; Mismatches 43; Indels 0;
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                      US-09-134-001C-1936/c
; Sequence 1936, Application US/09134001C
; Patent No. 6380370
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25-APR-1997
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CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
                                                                                                                                        4851 TGTGAAAGCTACC 4839
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy C
COMPUTER: IBM PC COMF
                                                                                              480 GATGATTTTYACC 492
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Sequence 5, Application US/09362642
Patent No. 6350935
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Bennett, Alan B.
APPLICANT: Rose, Jocelyn K.C.
APPLICANT: The Regents of the University of California
TITLE OF INVENTION: Fruit Specific and Ripening Regulation Expansin Genes
FILE REPERENCE: 023070-078210US
FULE REPERENCE: 023070-078210US
CURRENT APPLICATION NUMBER: US/09/362,642
CURRENT FILING DATE: 1999-07-27
NUMBER OF SEQ ID NOS: 8
                                                                                                                                                                                                                                                                                                                                238 GGCTATGACTTCAGCTACACTGGACAAACTGCTCTCTACAACCAGGCTGGATGCAGT 297
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6.5%; Score 31.8; DB 2; Length 537; 52.7%; Pred. No. 0.88; 1.ve 0; Mismatches 62; Indels (
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LOCATION: (1)..(537)
OTHER INFORMATION: melon expansin (CmEx1) partial cDNA clone
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RESULT 6
US-09-611-781-5
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REGISTRATION NUMBER: 26,742
REFERENCE/DOCKET NUMBER: 1340-1-013N
TELECOMMUNICATION INFORMATION:
TELEPHONE: 201-487-5800
TELEPHONE: 201-343-1684
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 6354 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                             Matches 103;
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Best Local Similarity
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Patent No. 6130065
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                                                                                                                                                                5759 GGAGAGGGGAGTTGGAGACCAGTATGAGCTGCAGCCGTTTCCCCTCCCAGGTCAGTTCTTC 5818
                                                                                                                                                                                                                                                                                                                                             5639
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ADDRESSEE: David A. Jackson, Esq.
STREET: 411 Hackensack Ave, Continental Plaza,
STREET: Floor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Patel, Divyen
TITLE OF INVENTION: A. TITLE OF INVENTION: (NBMPR)-INSENSITIVE, EQUILIBRATIVE, NUCLEOSIDE TRANSPORT
TITLE OF INVENTION: (NBMPR)-INSENSITIVE, EQUILIBRATIVE, NUCLEOSIDE TRANSPORT
TITLE OF INVENTION: PROTEIN, NUCLEIC ACIDS ENCODING THE SAME AND METHODS OF
TITLE OF INVENTION: USE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICATION NUMBER: US/09/1
FILING DATE: April 9, 1998
CLASSIFICATION: 800
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                   138
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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STATE: New Jersey
                                                                                                                                                                                                                                                                                                                                    CACCCTGTCCGTCTTCCCCGCCATCACAGCCATGGTGACCAGCTCCACCAGTCCTGGGAA 5698
                                                                                  AACCCCATCTGCTTCCTCCTCTTCAACATCATGGACTGG 5860
                                                                                                                     TGGAÇAAAÇTGCTGCTCTCTAÇAACCAGGCTGGATGCAGTGG 299
                                                                                                                                                                                                        ATATAGCAAGTGTGGATGCTCAGCTATACATCAGAAGGGGAGGCTATGACTTCAGCTACAÇ 257
                                                                                                                                                                                                                                                    GGTGAATGGGAGTGCATTTACAGTATGGAGTGGTCCAGGTTGTAACAACCGTGCTGAGCG 197
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                linear
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                                                                                                                                                                                                                                                                                                                                                                                                                                               46.4%;
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                                                                                                                                                                                                                                                                                                                                                                                                                      Score 31.6; DB 3; Pred. No. 3.7; 0; Mismatches 119;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DB 3; Length 6354;
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                                                                                                                                                                                                                                                                                                                         Matches
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Patent No. 6423829
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 09/058,389

FILING DATE: April 9, 1998

ATTORNEY/AGENT INFORMATION:

NAME: Jackson Esq., David A.

REGISTRATION NUMBER: 26,742

REFERENCE/DOCKET NUMBER: 1340-1-013N

TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TELEFAX: 201-343-1684
INFORMATION FOR SEQ ID NO: 5:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Patel, Di
TITLE OF INVENTION:
TITLE OF INVENTION:
TITLE OF INVENTION:
TITLE OF INVENTION:
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APPLICANT:
APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER READABLE FORM:
MEDIUM TYPE: Ploppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0,
CURRENT APPLICATION DATA:
                                                                                                                                                              5699
                                                                                                                                                                                                                                                                                                                                                                                                                      MOLECULE TYPE: HYPOTHETICAL:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE CHARACTERISTICS:
LENGTH: 6354 base pairs
5819 AACCCCATCTGCTGCTTCCTCCTCTTCAACATCATGGACTGG 5860
                                                                                                                                                                                                                                      5639 CACCCTGTCCGTCTTCCCCCGCCATCACAGCCATGGTGACCAGCTCCACCAGTCCTGGGAA 5698
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NUMBER OF SEQUENCES: 22
CORRESPONDENCE ADDRESS:
ADDRESSE: David A. Jackson, Esq.
STREET: 411 Hackensack Ave, Continental Plaza,
STREET: Floor
                                                                                                                   198 ATATAGCAAGTGTGGATGCTCAGCTATACATCAGAAGGGAGGCTATGACTTCAGCTACAC 257
                                                                                                                                                                                                                                                                                  78
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICATION NUMBER: US/09/611,781 FILING DATE:
                                                                                                                                                                                                                                                                                                                                         Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                               TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELEPHONE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ZIP: 07601
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CITY: Hackensack
                                TGGACAAACTGCTGCTCTCTACAACCAGGCTGGATGCAGTGG 299
                                                                              GTGGAGTGAGTGTCAGGGTGGAGAAGACGGCAGGGGGGGAACAAAGGGGAAGAACG
                                                                                                                                                                                               GGTGAATGGGAGTGCATTTACAGTATGGAGTGGTCCAGGTTGTAACAACCGTGCTGAGCG 197
                                                                                                                                                                                                                                                                           CACCAAGTTGTTCTTCTCAGTCATTACTGTGATGATGCTCATAGCAATGGCAAGTGAGAT 137
                                                                                                                                                                                                                                                                                                                   103;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                nucleic acid
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                                                                                                                                                                                                                                                                                                                     Conservative
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1: A NITROBENZYLMERCAPTOPURINERIBOSIDE
N: (NBMPR) -INSENSITIVE, EQUILIBRATIVE, NUCLEOSIDE TRANSPORT
N: PROTEIN, NUCLEIC ACIDS ENCODING THE SAME AND METHODS OF
                                                                                                                                                                                                                                                                                                                                     46.4%;
                                                                                                                                                                                                                                                                                                                 Score 31.6; DB 4; Pred. No. 3.7; 0; Mismatches 119;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Version
                                                                                                                                                                                                                                                                                                                                                      Length 6354;
                                                                                                                                                                                                                                                                                                                     Indels
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US-08-724-394A-20/c

Sequence 20, Application US/08724394A Patent No. 5872237

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Db 144976 Caracaratriadcacdiridesesesekeletaratrarateseseseseseagisca 144917
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         131 GTGAGATGGTGAATGGGAGTGCATTTACAGTATGGAGTGGTCCAGGTTGTAACAACCGTG 190
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DB 2; Length 246240;
                                                                                                                                                                           TITLE OF INVENTION: Megabase Transcript Map: No. 5872237el TITLE OF INVENTION: Sequences and Antibodies Thereto
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 76; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA: APPLICATION NUMBER: US/08/724,394A FILING DATE: 01-OCT-1996 CLASSIFICATION: 536
                                                                                                                                                                                                                     NUMBER OF SEQUENCES: 31
CORRESPONDENCE ADDRESS:
ADDRESSEE: TOWNSEND and TOWNSEND and CREW LLP
STREET: Two Embarcadero Center, 8th Floor
CITY: San Francisco
STATE: CA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Db 144916 TTCACAATGGATAAACACGTGTAATATACCTCC 144884
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 6.4%; Score 31.4; D. 50.3%; Pred. No. 28; tive 0; Mismatches
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| LOCATION: 1..246240

| OTHER INFORMATION: /note= "HLA-H.CONTIG'

US-08-724-394A-20
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US-08-724-394A-21/C
US-08-724-394A-21/C
Sequence 21, Application US/08724394A
Patent No. 5872237
APPLICANT: Feder, John N.
APPLICANT: Kronmal, Gregory S.
APPLICANT: Lauer, Peter M.
APPLICANT: Ruddy, David A.
                                                                                                                                                                                                                                                                                                                                                                         ZIP: 94111-3834
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CLASSIFICATION: 536
ATTORNEY/ACENT INFORWATION:
NAME: Fitch, Renee A: 826.136
REFTERENCE/DOCKET NUMBER: 01795
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-576-0200
INFORMATION FOR SEQ ID NO: 20: SEQUENCE CHARACTERISTICS:
LENGTH: 246240 base pairs
                                            Kronmal, Gregory S.
Lauer, Peter M.
Ruddy, David A.
                                                                                                          Thomas, Winston
Tsuchihashi, Zenta
Wolff, Roger K.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: nucleic acid STRANDEDNESS: not relevant TOPOLOGY: not relevant MOLECULE TYPE: cDNA
                       Feder, John N.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity 50.33
Matches 77; Conservative
GENERAL INFORMATION:
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APPLICANT:
APPLICANT:
APPLICANT:
APPLICANT:
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                                              APPLICANT
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Db 145036 GGGAGAAGGAGCAGGTTGGTTATŤTTATGCCTCATAGGCTATATATATACACAATAGAGT 144977
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       191 CTGAGCGATATAGCAAGTGTGGATGCTCAGCTATACATCAGAAGGGAGGCTATGACTTCA 250
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0; Gaps
APPLICANT: Thomas, Winston
APPLICANT: Tsuchihashi, Zenta
APPLICANT: Wolff, Roger K.
TITLE OF INVENTION: Megabase Transcript Map: No. 5872237e1
TITLE OF INVENTION: Squences and Antibodies Thereto
NUMBER OF SEQUENCES: 31
CORRESPONDENCE ADDRESS:
ADDRESSEE: TOWNSEND and TOWNSEND and CREW LLP
STREET: Two Embarcadero Center, 8th Floor
CITY: San Francisco
CITY: CAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
6.4%; Score 31.4; DB 2; Length 246240;
Best Local Similarity 50.3%; Pred. No. 28;
Matches 77; Conservative 0; Mismatches 76; Indels 0;
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Sequences and Antibodies Thereto
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/724,394A
FILING DATE: 01-0CT-1996
CLASSIFICATION: 536
ATTONNEY/AGENT INFORMATION:
NAME: Fitts, Renee A.
REGISTRATION NUMBER: 35,136
REFERENCE/DOCKET NUMBER: 017957-000100
TELEPHONE: 415-576-0200
TELEPHONE: 415-576-0300
INFORMATION FOR SEQ ID NO: 21:
SEQUENCE CHARACTERISTICS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ; NAME/KEY: misc_feature
; LCGATION: 1..246240
; OTHER INFORMATION: /note= "HLA-H.CONTIG"
US-08-724-394A-21
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US-08-724-394A-22/c
Sequence 22, Application US/08724394A
Parent No. 5872237
                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
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Lauer, Peter M.
Ruddy, David A.
Thomas, Winston
Teuchihashi, Zenta
Wolff, Roger K.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LENGTH: 246240 base pairs
TYPE: nucleic acid
STRANDEDNESS: not relevant
TOPOLOGY: not relevant
                                                                                                                                                                                                                                                                                                                                                                                                                     Floppy disk
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                                                                                                                                                                                                                                                                                                                                                              ZIP: 94111-3834
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: TSUCHIHA APPLICANT: Wolff, R. TITLE OF INVENTION: TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GENERAL INFORMATION:
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APPLICANT:
APPLICANT:
APPLICANT:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Db 144916 TTCACAATGGATAAACACGTGTAATATACCTCC 144884
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ; NAME/KEY: misc_feature
; LOCATION: 1.246240
; OTHER INFORMATION: /note= "HLA-H.CONTIG"
US-08-724-394A-22
                                                                                                                                                                                                                                                                                                                                                                                    US-07-741-453A-57/c
                                                                                                                                                                                                                                                                                                               Sequence 57, Application US/07741453A Patent No. 6228597 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 6.4%;
Best Local Similarity 50.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Matches
                                                                              APPLICANT: LIBERT, FREDERIC
APPLICANT: DUMONT, JACQUES
APPLICANT: VASSART, GILBERT
TITLE OF INVENTION: POLYPEPTIDES HAVING
TITLE OF INVENTION: ACTIVITY, NUCLEIC ;
TITLE OF INVENTION: AND POLYPEPTIDES, ;
NUMBER OF SEQUENCES, 62
CORRESPONDENCE ADDRESS:
ADDRESSEE: CUSHMAN DARBY & CUSHMAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELEFAX: 415-576-0300
INFORMATION FOR SEQ ID NO: 22:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           REFERENCE/DOCKET NUMBER: 01
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-576-0200
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CLASSIFICATION: 536
ATTORNEY/AGENT INFORMATION:
NAME: Fitts, Renee A.
REGISTRATION NUMBER: 35,1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NUMBER OF SEQUENCES: 31
CORRESPONDENCE ADDRESS:
ADDRESSEE: TOWNSEND and TOWNSEND and CREW LLP
STREET: Two Embarcadero Center, 8th Floor
                                                                                                                                                                                                                                                                                       APPLICANT:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     131 GTGAGATGGTGAATGGGAGTGCATTTACAGTATGGAGTGGTCCAGGTTGTAACAACCGTG 190
                                     STREET: 1615 L STREET, N.W. CITY: WASHINGTON, D.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LENGTH: 246240 base pairs
TYPE: nucleic acid
STRANDEDNESS: not relevant
TOPOLOGY: not relevant
                     COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STREET: Two Embarca
CITY: San Francisco
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FILING DATE: 01-OCT-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CTGAGCGATATAGCAAGTGTGGATGCTCAGCTATACATCAGAAGGGAGGCTATGACTTCA 250
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GCTACACTGGACAAACTGCTGCTCTACAACC 283
20036
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                                                                                                                                                                                                                                                                                          PARMENTIER, MARC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Conservative
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                                                                                                                                              POLYPEPTIDES HAVING THYROTROPIN-RECEPTOR
ACTIVITY, NUCLEIC ACID SEQUENCES CODING FOR SUCH RECEPTORS
AND POLYPEPTIDES, AND APPLICATIONS OF THESE POLYPEPTIDES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                US/08/724,394A
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Pred. No. 28;
0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0; Gaps
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US-08-121-446-3/c
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TELEFAX: (202) 822-0944
TELEX: 6714627 CUSH
INFORMATION FOR SEQ ID NO: 57
SEQUENCE CHARACTERISTICS:
LENGTH: 4417 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 3, Application US/08121446
Patent No. 6313276
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Matches 108;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity
                                                                                           COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
COFFMANDE: Bateaut Dalage #1 0
                                                                                                                                                                                                                                                                                                                                     APPLICANT: IMURA, HIROO
APPLICANT: NAKAO, KAZUWA
APPLICANT: NAKANISHI, SHIGETADA
TITLE OF INVENTION: A HUMAN ENDOTHELIN RECEPTOR
NUMBER OF SEQUENCES: 4
                                                              SOFTWARE: PatentIn Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TOPOLOGY: linear MOLECULE TYPE: cDNA
                                                                                                                                                                                                                                                                                                                     CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NAME: KOKULIS, PAUL N.
REGISTRATION NUMBER: 16773
REFERENCE/DOCKET NUMBER: 91
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 861-3000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ATTORNEY/AGENT INFORMATION:
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CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/741,453A
FILING DATE: 19911015
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER READABLE FORM:
MEDIUM TYPE: Disk
COMPUTER: IBM PC com
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    319 TCTATTGACAAGTAGATCCTGGAAATATTGGGCAGATTTGAAAATGCACGACTGGG 264
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   379
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                                                                                                                                                                                                                                                                             STREET:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  205 AAGTGTGGATGCTCAGCTATACATCAGAAGGGAGGCTATGACTTCAGCTACACTGGACAA 264
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       145 GGGAGTGCATTTACAGTATGGAGTGGTCCAGGTTGTAACAACCGTGCTGAGCGATATAGC
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APPLICATION NUMBER: US/08/121,446 FILING DATE: CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        85 TTGTTCTTCTCAGTCATTACTGTGATGATGCTCATAGCAATGGCAAGTGAGATGGTGAAT 144
                                                                                                                                                                                              ZIP: 94304-1018
                                                                                                                                                                                                                                  CITY: Palo Alto
STATE: California
                                                                                                                                                                                                                                                                                                     ADDRESSEE:
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TYPE: NUCLEIC ACID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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                                                                                                                                                                                                                                                                             755 Page Mill Road
                                                                                                                                                                                                                  USA
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Pred. No. 4.1;
0; Mismatches 128; Indels
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Db 106735 ACAGGCATAAAATATATATATATACTTAAAACCAAGGTTTTCA 106693
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SEQ ID NO 9
LENGTH: 3715
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US-08-973-462-2/c
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APPLICANT: GUEGLER, Karl et al
APPLICANT: GUEGLER, Karl et al
APPLICANT: GUEGLER, Karl et al
TITLE OF INVENTION: ISOLATED HUMAN PROTEASE PROTEINS,
TITLE OF INVENTION: USES THEREOF
FILE REPERENCE: CL000968
CURRENT APPLICATION NUMBER: US/09/741,150
CURRENT FILING DATE: 2000-12-21
NUMBER OF SEQ ID NOS: 4
SOFTWARE: FRAELSEQ for Windows Version 4.0
SEQ ID NO 3
SEQ ID NO 3
SEQ ID NO 3
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match 6.3%; Score 31; DB 4; Length 4301; Best Local Similarity 51.0%; Pred. No. 4.7; Matches 73; Conservative 0; Mismatches 70; Indels
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                                                                                                                                            29900-20324.00
                        APPLICATION NUMBER: US 07/911,684
FILING DATE: 10-07U-1992
ATTORNEY/AGENT INFORMATION:
NAME: CIOTTI, THOMAS E.
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| OTHER INFORMATION: n = A,T,C or G
US-09-741-150-3
                                                                                       NAME: CIOTTI, THOWAS E.
REGISTRATION NUMBER: 21,013
REFERENCE/OCKET UNMBER: 2990
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 813-5600
TELEPHONE: (415) 494-0792
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         464 TACGGTATCACCATGTGATGTT 486
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                                                                                                                                                                                                                                 TELEX: 706141
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                        LENGTH: 4301 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
    PRIOR APPLICATION DATA:
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238..1566
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ORGANISM: Human
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                                                                                                                                                                                                                                                                                                                                                                                                                            ; NAME/KEY:
; LOCATION:
US-08-121-446-3
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APPLICANT: DRUILHE, PIERRE
APPLICANT: DRUILHE, PIERRE
TITLE OF INVENTION: MALARIAL PRE-ERYTHROCYTIC STAGE POLYPEPTIDE MOLECULES
FILE REFERENCE: 0660-0125-0 PCT
CURRENT APPLICATION NUMBER: US/08/973,462B
CURRENT FILING DATE: 1996-02-06
EARLIER APPLICATION NUMBER: PCT/FR96/00894
EARLIER FILING DATE: 1996-06-12
EARLIER FILING DATE: 1995-06-13
NUMBER OF SEQ ID NOS: 29
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      6.2%; Score 30.8; DB 4; Length 3715; ilarity 61.0%; Pred. No. 5.1; Conservative 0; Mismatches 32; Indels 0;
                                                          GENERAL INFORMATION:
APPLICANT: Yamanouchi Pharmaceutical Co., Ltd.
TITLE OF INVENTION: A novel potassium channel protein
FILE REFERENCE: Y9903-PCT
CURRENT APPLICATION NUMBER: US/09/600,776
CURRENT FILING DATE: 2000-07-21
PRIOR APPLICATION NUMBER: UP P1998-011434
PRIOR RILING DATE: 1998-01-23
PRIOR FILING DATE: 1998-01-23
PRIOR FILING DATE: 1998-12-04
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Sequence 9, Application US/09600776
Patent No. 6326168
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    293 GCAGTGGTGTTGCACACACCAG 314
                                                                                                                                                                                                                                                                                                                                                                 NUMBER OF SEQ ID NOS: 12
SOFTWARE: Patentin Ver. 2.0
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SEQ ID NO 2
LENGTH: 5361
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; LOCATION: (1)..(5361)
US-08-973-462-2
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Best Local Similarity
Matches 50; Conserv
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RESULT 15
US-08-973-462-1/c
| Sequence 1, Application US/08973462B
| Patent No. 6191270
| GENERAL INFORMATION:
| APPLICANT: DAUBERSIES, PIERRE
| APPLICANT: DAUBERSIES, PIERRE
| TITLE OF INVENTION: MALARIAL PRE-ERYTHROCYTIC STAGE POLYPEPTIDE MOLECULES
| FILE REFERENCE: 0660-0125-0 PCT
| CURRENT APPLICATION NUMBER: US/08/973,462B
| CURRENT FILING DATE: 1998-02-06
| EARLIER APPLICATION NUMBER: PCT/FR96/00894
| EARLIER FILING DATE: 1996-06-12
| EARLIER FILING DATE: 1995-06-13
| NUMBER OF SEQ ID NOS: 29
| SOPTWARE: PATENTIN OLYTE: 1995-06-13
| NUMBER OF SEQ ID NOS: 29
| SOFTWARE: PATENTIN Ver. 2.0
| TYPE: DNA
| ORGANISM: P. falciparum
| US-08-973-462-1
Search completed: January 12, 2003, 08:42:01 Job time : 365 secs
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6.2%; Score 30.6; DB 4; Length 6152;
Best Local Similarity 52.0%; Pred. No. 7.7;
Matches 66; Conservative 1; Mismatches 60; Indels 0; Gaps
                                                                                                                                                                                  5428 ATGITTTAAATTCTTAAAGATATCAAATACAAATGAATAAAACGGTCTCTCCTTATTTTT 5369
                                                                                                                                                                                                                                                                           5488 TACTTCTATTACATTATTTATTTTTTCTTTACTAAATTTTTCTTTCATTTGTTAAATA 5429
                                                                                           5368 ATTTATA 5362
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                                                                                                                                                                                                                  424 ATTAGAGAGATGCATGGATATAATAAATAAGTAAAAGCTAACGGTATCACCATGTGATG 483
                                                                                                                                                                                                                                                                                                            364 TTCATCCAATGCTAGATITCATAACTCTTGGATCCATCTTCTATGTTTTTCAAGTGTATA 423
                                                                                                                                        484 ATTTTYA 490
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Result
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Maximum Match 100%
Listing first 45 summaries
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Maximum DB seq length: 2000000000
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US-09-764-864-168
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Sequence 6488, Ap
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Sequence 1, Appli
Sequence 10265, A
Sequence 9535, Ap
Sequence 168, App
Sequence 644, App
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US-09-882-434A-2

Sequence 2, Application US/09882434A Patent No. US20020108144A1 GENERAL INFORMATION:

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Sequence 11947, A Sequence 13309, A	Sequence 3496, Ap	Sequence 3485, Ap	•	Sequence 380, App	Sequence 1, Appli				Sequence 825, App		Sequence 2038, Ap	Sequence 3659, Ap	Sequence 2045, Ap	Sequence 11395, A	Sequence 714, App	Sequence 714, App	Sequence 714, App	Sequence 1, Appli	Sequence 5512, Ap	Sequence 1, Appli	Sequence 4, Appli	Sequence 114, App		Sequence 2062, Ap

ALIGNMENTS

APPLICANT: Manners, John M.
APPLICANT: Marcus, John Paul
APPLICANT: Green, Jodie Lyn
TITLE OF INVENTION: ANTI-MICROBIAL PROTEIN
FILE REFERENCE: CULLN18:1CP1C1
CURRENT APPLICATION UNMBER: US/09/882,434A
CURRENT FILING DATE: 2001-06-15
PRIOR APPLICATION NUMBER: 09/364395
PRIOR APPLICATION NUMBER: 09/364395
PRIOR APPLICATION NUMBER: 09/117615
PRIOR APPLICATION NUMBER: 09/117615
PRIOR APPLICATION NUMBER: PCT/AU97/00052
PRIOR APPLICATION NUMBER: PCT/AU97/00052
PRIOR FILING DATE: 1999-01-31

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SEQ ID NO 2

PRIOR APPLICATION NUMBER: AU PN 7802
PRIOR FILING DATE: 1996-01-31
NUMBER OF SEQ ID NOS: 21
SOFTWARE: FASTSEQ for Windows Version 4.0

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Query Match
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Sequence (488, Application US/09864761
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GENERAL INFORMATION:
APPLICANT: Penn, Sharron G.
APPLICANT: Penn, Sharron G.
APPLICANT: Penn, Sharron G.
APPLICANT: Hand, David R.
APPLICANT: HANGE CONTROLL OF SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR TITLE OF INVENITION: GENE EXPRESSION ANALYSIS BY MICROARRAY FILE SEPRENCE: Acomica x 1 2001-05-23
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61 ACCTCAGCCATGGCTTCCACCAAGTTGTTCTTCTCAGTCATTACTGTGATGATGCTCATA
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APPLICANT: WEI, MING-Hui et al
TITLE OF INVENTION: ISOLATED HUMAN TRANSPORTER PROTEINS,
TITLE OF INVENTION: ISOLATED HUMAN TRANSPORTER PROTEINS,
TITLE OF INVENTION: AND USES THEREOF
FILE REFERENCE: CLOOLOIB
CURRENT PAPLICATION NUMBER: US/09/734,674
CURRENT FILING DATE: 2000-12-13
NUMBER OF SEQ ID NOS: 4
SOFTWARE FRANSE FRANSPORTER PROTEINS,
LENGTH: 202001
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             6.6%; Score 32.4; DB 10; Length 463; 60.0%; Pred. No. 2.4; tive 0; Mismatches 36; Indels 0
                                                                                                                                                                                                                                                                                                                                                                                     TYPE: DNA

ORGANISM: Homo sapiens

FEATURE:

OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 2.4

OTHER INFORMATION: EXPRESSED IN HEART, SIGNAL = 2.5

OTHER INFORMATION: EXPRESSED IN HEART, SIGNAL = 2.5

OTHER INFORMATION: EXPRESSED IN HEART, SIGNAL = 2.5

OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 2.5

OTHER INFORMATION: EXPRESSED IN HELA, SIGNAL = 2.7

OTHER INFORMATION: EXPRESSED IN HELA, SIGNAL = 2.5

OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 2.5

OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 2.5

US-09-864-761-6488
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PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/USO1/00670
PRIOR FILING DATE: 2001-01-30
PRIOR FILING DATE: 2000-09-21
PRIOR FILING DATE: 2000-09-21
PRIOR FILING DATE: 2000-06-30
PRIOR FILING DATE: 2000-06-30
PRIOR FILING DATE: 2001-01-29
NUMBER: OF SEQ ID NOS: 49117
SOFTWARE: Annowax Sequence Listing Engine vers. 1.1
SEQ ID NO 6488
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         324 CAGTGCCAGGGCATGCAACCCTTTTGGTTG 353
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                212 CAGTGGCAGGGAAGGGATAAATAAAAGTTG 241
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ORGANISM: Human
FEATURE:
NAME/KEY: misc_feature
LCCATION: (1)...(202001)
OTHER INFORMATION: n = A,T,C or G
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              54; Conservative
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Matches 59; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Best Local Similarity
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US-09-734-674-3/c
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APPLICANT: AGlate, Paul A.

APPLICANT: Jones, Robert

APPLICANT: Hallocker, Suean L.

TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY

TITLE OF INVENTION: COMPOSITIONS OF OVARIAN CANCER

FILE REFERENCE: 210121.497

CURRENT APPLICATION NUMBER: US/09/867,701

CURRENT FILING DATE: 2001-05-29

NUMBER OF SEQ ID NOS: 10912

SOFTWARE: FASTSEQ for Windows Version 4.0

SEQ ID NO 10265

LENGTH: 133

TYPE: DNA

ORGANISM: Homo sapien
                                                                                                                                                                                                                                                                                                                                                                                                                                                              US-09-867-701-10265/c
; Sequence 10265, Application US/09867701
; Patent No. US20020132237A1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Db 307902 AATGGTGGCCTCTAACAAGGCTGGGTTCTGGTACTGCTGGCTCCTTATTCTACGGCCCAC 307843
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                                                                                                US-09-867-701-10265
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PRIOR FILING DATE: 2000-02-22
PRIOR APPLICATION NUMBER: 09/692414
PRIOR FILING DATE: 2000-10-20
PRIOR APPLICATION NUMBER: 09/768184
PRIOR FILING DATE: 2001-01-24
PRIOR APPLICATION NUMBER: 09/804076
PRIOR APPLICATION NUMBER: 09/804076
PRIOR APPLICATION NUMBER: 09/826314
PRIOR APPLICATION NUMBER: 09/826314
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                              GENERAL INFORMATION:
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                                                  Query Match
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SOFTWARE: FastSEQ for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CURRENT APPLICATION NUMBER: US/09/933,267A CURRENT FILING DATE: 2001-08-21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Kalush, Francis et al.
TITLE OF INVENTION: Estrogen receptor alpha variants and
TITLE OF INVENTION: methods of detection thereof
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FILE REFERENCE: CL000258CI4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRIOR FILING DATE: 2001-04-05
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRIOR FILING DATE: 1999-10-20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRIOR APPLICATION NUMBER: 60/160626
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LENGTH: 465237
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          415
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              355 AAGAGTATCTTCATCCAATGCTAGATTTCATAACTCTTGGATCCATCTTCTATGTTTTTC 414
  Local Similarity 56.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAGTGTATAATTAGAGAGATGCATGGATATATAATA 450
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                   6.4%; Score 31.6; DB 10; 56.9%; Pred. No. 2.2;
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0;
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  Mismatches
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44;
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                                             Length 133;
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0
Gaps
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0
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APPLICANT: Byatt, John C.

APPLICANT: Mathialagan, Nagappan

TITLE OF INVENTION: MUCLEIC ACID AND OTHER MOLECULES ASSOCIATED WITH LACTATION J.

FILE REPERENCE: 16511.006/37-21(10298)C

CURRENT APPLICATION NUMBER: US/09/960,352

CURRENT FILING DATE: 2001-09-24

NUMBER OF SEQ ID NOS: 15112

LENGTH: ? ? .
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; TYPE: DNA
; ORGANISM: Bos taurus
; OTHER INFORMATION: Clone ID: 41-LIB3058-026-Q1-K1-C2
US-09-960-352-9535
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 168, Application US/09764864 Patent No. US20020132753A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                  Prior application data removed - consult PALM or file wrapper NUMBER OF SEQ ID NOS: 1792
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 168
                                                                                                                                             Matches
                                                                                                                                                                                  Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Rosen et al. TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies FILE REFERENCE: PTZ23
CURRENT APPLICATION NUMBER: US/09/764,864
CURRENT FILING DATE: 2001-01-17
                                                                                                                                                                                                                                          ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                             LENGTH: 614
TYPE: DNA
288 TGGATGCAGTGGTGTTGCACA 308
                                                          353 TCAGAGAGTTGGCTACAACTTCTGCTGCACTGAACACACTGGTAGGGTTTCTCCTCAGCA 294
                                                                                     228 TCAGAAGGGAGGCTATGACTTCAGCTACACTGGACAAACTGCTGCTCTCTACAACCAGGC 287
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  360 TATCTTCATCCAATGCTAGATTTCATAACTCTTGGATCCATCTTCTATGTTTTTCAAGTG 419
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              111 TTTTATTAAATAAATATATAAAAGTTTTTTAATCTATATTAAAATATTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   439 GGATATATAATAAATAAGTAAAAGCTACGGTATCACCATGTGATGATTT 487
                                                                                                                                                             Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            . Match 6.4%;
Local Similarity 61.5%;
Les 67; Conservative
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                                                                                                                                             Conservative
                                                                                                                                                             6.4%;
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                                                                                                                                        Score 31.4; DB Pred. No. 5.8; 0; Mismatches
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                                                                                                                                                                                Length 614;
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US-09-754-853A-3/c
; Sequence 3, Application US/09754853A
; Sequence 3, Application US/09754853A
; Publication No. US2030005491A1
; GENERAL INFORMATION:
; APPLICANT: Hauge, Brian M.
; APPLICANT: Parenell, Laurence D.
; APPLICANT: Parenell, Laurence D.
; APPLICANT: Parenell, Laurence D.
; APPLICANT: Parenell, Laurence D.
; APPLICANT: Wang, Ming Li
; TILLE OF INVENTION: Notleic Acid Molecules And Other Molecules Associated With
; TILLE OF INVENTION: Soybean Cyst Nematode Resistance
; FILE REFERENCE: 38-10(15610) B
; CURRENT APPLICATION NUMBER: US/09/754,853A
; CURRENT PILING DATE: 2000-01-05
; PRIOR FILING DATE: 2000-01-07
; NUMBER OF SEQ ID NOS: 1119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Db 185216 TTTTTCATAAGCTAGAATTTCTATCTATTAGTTTCTTCAAAAATTATTTCTAACTTATG 185157
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                                                         Db 185216 TTTTTCATAAGCTAGAATTTCTATCTATTAGTTTCTTCAAAAATTATTTCTAACTTATG 185157
                                                                                                                                                                                       424 ATTAGAGAGATGCATGGATATATAATAATAAGTAAAGCTACGGTATCACCATGTGATG 483
                                                                                                                          424 ATTAGAGAGATGCATGGATATAATAATAAGTAAAGCTACGGTATCACCATGTGATG 483
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364 TTCATCCAATGCTAGATTTCATAACTCTTGGATCCATCTTCTATGTTTTTCAAGTGTATA 423
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APPLICANT: Nakao, Kazuwa
APPLICANT: Nakao, Kazuwa
APPLICANT: Nakao, Kazuwa
APPLICANT: Nakao, Human Endothelin Receptor
TITLE OF INVENTION: Human Endothelin Receptor
CURRENT APPLICATION NUMBER: US/09/931,157
CURRENT FILING DATE: 2090-10-15
PRIOR APPLICATION NUMBER: 08/121,446
PRIOR APPLICATION NUMBER: 07/911,684
PRIOR FILING DATE: 1992-00-14
PRIOR FILING DATE: 1992-07-10
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LOCATION: (46798)..(48763),(48975)..(49573)

TOTHER INFORMATION: Clone ID: 240017_region_G3

US-09-754-853A-3
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: DNA ORGANISM: Glycine max
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Db 185096 Arrirr 185091
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US-09-931-157-2/c
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1 Sequence 2, Application US/09754853A

1 Sequence 2, Application US/09754853A

2 Publication No. US2030005491A1

3 GENERAL INFORMATION:

APPLICANT: Hauge, Brian M.

APPLICANT: Parnell, Laurence D.

APPLICANT: Wang, Ming Li

TITLE OF INVENTION: Nucleic Acid Molecules And Other Molecules Associated With

TITLE OF INVENTION: Nucleic Acid Molecules And Other Molecules Associated With

TITLE OF INVENTION: Nucleic Acid Molecules And Other Molecules Associated With

TITLE OF INVENTION: Soybean Cyst Nematode Resistance

TITLE OF INVENTION: Soybean Cyst Nematode Resistance

TITLE OF INVENTION: Soybean Cyst Nematode Resistance

CURRENT FILING DATE: 2001-01-05

PRIOR PELICATION NUMBER: US 60/174,880

PRIOR PELICATION NUMBER: US 60/174,880

NUMBER OF SEQ ID NOS: 1119

SEQ ID NO 2

LENGTH: 335913
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: LOCATION: (45163) .. (45314), (45450) .. (45509), (46941) .. (48763), (48975) .. (49573)
; OTHER INFORMATION: Clone ID: 240017_region_G3
US-09-754-853A-2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     228 TCAGAAGGGAGGCTATGACTTCAGCTACACTGGACAAACTGCTGCTCTCTACAACCAGGC 287
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
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6.3%; Score 31.2; DB 9; Length 335913;
Best Local Similarity 52.4%; Pred. No. 1.7e+02;
Matches 66; Conservative 1; Mismatches 59; Indels 0;
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6.4%; Score 31.4; DB 10; Length 638;
Best Local Similarity 61.7%; Pred. No. 5.9;
Matches 50; Conservative 0; Mismatches 31; Indels 0
                                                                                                                                                                                                                                                    APPLICANT: Rosen et al.

TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies FILE REFERENCE: PT223

FULE REFERENCE: PT223

CURRENT APPLICATION NUMBER: US/09/764,864

CURRENT FILING DATE: 2001-01-17

Prior application data removed - consult PALM or file wrapper NUMBER OF SEQ ID NOS: 1792

SOFTWARE: Patentin Ver. 2.0

SEQ ID NO 604

LENGTH: 638
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LOCATION: (15)
OTHER INFORMATION: n equals a,t,g, or c
NAME/KEY: SITE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LOCATION: (43)
COTHER INFORMATION: n equals a,t,g, or c
US-09-764-864-604
                                                                                                                                                        ; Sequence 604, Application US/09764864; Patent No. US20020132753A1; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       288 TGGATGCAGTGTTGCACA 308
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    345 recentrerecienterana 325
293 TGGGTTTTCTGGTGTTCAATA 273
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                                                                                                                          US-09-764-864-604/c
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APPLICANT: Marcus, John Paul
APPLICANT: Goulter, Kenneth C.
APPLICANT: Green, Jodie Lyn
TITLE OF INVENTION: ANTI-MICROBIAL PROTEIN
FILE REFERENCE: CULLN18.1CPLC1
CURRENT APPLICATION UNMBER: US/09/882,434A
CURRENT FILING DATE: 2001-06-15
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US-09-882-434A-2/c
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Best Local Similarity
Thes 73; Conserva
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; LOCATION: (238)...(1566)
US-09-931-157-2
                                                                                                                                                                                                                                                                                                                                                                                                                PRIOR APPLICATION NUMBER: 09/364395
PRIOR FILING DATE: 1999-07-30
PRIOR APPLICATION NUMBER: 09/117615
PRIOR FILING DATE: 1998-11-09
PRIOR APPLICATION NUMBER: PCT/AU97/00052
PRIOR FILING DATE: 1997-01-31
PRIOR APPLICATION NUMBER: AU PN 7802
PRIOR FILING DATE: 1996-01-31
PRIOR FILING DATE: 1996-01-31
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SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 2
                                                                                                                                                            Query Match
Best Local :
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                                                                                                                                             Matches
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PRIOR FILING DATE: 1991-07-12
NUMBER OF SEQ ID NOS: 2
                                                                                                                                                                                                                             NAME/KEY: CDS
LOCATION: (70)...(375)
OTHER INFORMATION: y=t or c.
                                                                                                                                                                                                                                                                                                TYPE: DNA
ORGANISM: Macadamia integrifolia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SOFTWARE: FastSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: DNA
ORGANISM: Homo Sapiens
                                                                                                                                                                                                                                                                                          FEATURE:
                                                                                                                                                                                                                                                                                                                                                 LENGTH: 493
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    3613 GTGTGTAGTTTCAAAATTTGGCAAGATAATTAGAGAACATGATACTGACATGGAGAAGGA 3554
279 CAACCAGGCTGGATGCAGTGTTTGCACACACCAGGTTTTGGGTCCAGTGCCAGGGCATG 338
                                                        364 AGATACTCTTCCAACCAAAAGGGTTGCATGCCCTGGCACTGGACCCAAACCTGGTGTGT 305
                                                                                                        219
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                                                                                                                                                            Local Similarity
                                                                                            AGCTATAÇATÇAGAAGGGAGGCTATGACTTÇAGCTAÇAÇTGGAÇAAACTGCTGCTCTCTA 278
                                                                                                                                       74;
                                                                                                                                       Conservative
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                                                                                                                                                       6.2%;
50.7%;
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51.0%;
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                                                                                                                                                   Score 30.8; DB 10;
Pred. No. 7.8;
                                                                                                                                       Mismatches 72;
                                                                                                                                                                      Length 493;
                                                                                                                                     Indels
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US-09-929-230-3/c
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 3, Application US/09929230 Patent No. US20020161203A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity
Matches 50; Conserv
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APPLICANT: Yamanouchi Pharmaceutical Co., Ltd.
TITLE OF INVENTION: A novel potassium channel protein
FILE REFERENCE: Y9903-PCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 9, Application US/09965830 Patent No. US20020177201A1
                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Sheppard, Paul O.
APPLICANT: Bishop, Paul D.
TITLE OF INVENTION: RATTLESNAKE VENOM GLAND PROTEINS
FILE REFERENCE: 00-72
CURRENT APPLICATION NUMBER: US/09/929,230
CURRENT FILING DATE: 2001-08-13
NUMBER OF SEQ ID NOS: 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CURRENT APPLICATION NUMBER: US/09/965,830
CURRENT FILING DATE: 2001-10-01
PRIOR APPLICATION NUMBER: 09/600,776
PRIOR FILING DATE: 2001-07-21
PRIOR APPLICATION NUMBER: JP P1998-346198
PRIOR APPLICATION NUMBER: JP P1998-346198
PRIOR FILING DATE: 1998-12-04
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NUMBER OF SEQ ID NOS: 12
                                                                                                                                                                                                                                                        TYPE: DNA ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: DNA
ORGANISM: Rattus sp
                                                                                                                                                                                                                                                      FEATURE
                                                                                                                                                                                                                                                                                                           ENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LENGTH: 3715
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2772 AGTGAGGCAAGAAACACAGACACACTGGACAAGCTACGGCAGGCGGTGACGGAGCTGTCT 2831
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              293 GCAGTGGTGTTGCACACCAC 314
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          233 AGGGAGGCTATGACTTCAGCTACACTGGACAAACTGCTGCTCTCTACAACCAGGCTGGAT 292
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      244 CATAGCCTCCCTTCTGATGTATAGCT 219
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           304 CAACACCACTGCATCCAGCCTGGTTGTAGAGAGCAGCAGTTTGTCCAGTGTAGCTGAAGT 245
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CAACCCTTTTGGTTGGAAGAGTATCT 364
                                                                                                                                                                                                                                                                                                         453
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Pred. No. 23;
0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                             124 ATGCCAAGTGAGAGGGAGAGTGCATTTACAGTATGGAGTGGTCCAGGTTGTAAC 183
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              205 ANGCYTCYTCNSWNSWRTGDAINSWNGCNARNCKNSWRTCNCKRTGYTGNGTRTARC 146
                                                                                                                                                                                                            265 CYTINARNCCDATCCACAINSWNGTRAAYTINARNGTYTGNSWNGCNARYTINCCNACRA 206
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        184 AACCGTGCTGAGCGATATAGCAAGTGTGGATGCTCAGCTATACATCAGAAGGGAGGCTAT 243
                                                                                                                                                                                                                                                                                                                      64 TCAGCCATGGCTTCCACCAAGTTGTTCTTCTCAGTCATTACTGTGATGATGCTCATAGCA 123
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                                                                                     Gaps
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Query Match
6.2%; Score 30.6; DB 9; Length 453;
Best Local Similarity 26.3%; Pred. No. 8.6;
Matches 67; Conservative 47; Mismatches 141; Indels
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6.2%; Score 30.6; DB 10; Length 2;
Best Local Similarity 55.0%; Pred. No. 20;
Matches 60; Conservative 0; Mismatches 49; Indels
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FILE REFERENCE: P2022P1
FURRENT APPLICATION NUMBER: US/09/739,907
CURRENT FILING DATE: 2000-12-20
FRIOR APPLICATION NUMBER: 09/348,457
PRIOR APPLICATION NUMBER: 00/070,567
PRIOR FILING DATE: 1999-07-07
PRIOR APPLICATION NUMBER: 60/070,692
PRIOR FILING DATE: 1998-01-07
PRIOR FILING DATE: 1998-01-07
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PRIOR FILING DATE: 1998-01-07
PRIOR PAPELICATION NUMBER: 60/070,658
PRIOR FILING DATE: 1998-01-07
PRIOR FILING DATE: 1998-01-07
PRIOR PRIOR PAPELICATION NUMBER: 50070,658
PRIOR FILING DATE: 1998-01-07
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LOCATION: (1846)
OTHER INFORMATION: n equals a,t,g, or c
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LOCATION: (1246)
OTHER INFORMATION: n equals a,t,g, or c
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Patent No. US20010012889A1
GENERAL INFORMATION:
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Search completed: January 12, 2003, 09:41:31
Job time : 485 secs
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                                          Email: rosswhet@unity.ncsu.edu
Seg primer: 5′ lambda TriplEx2 Sequencing Primer.
Location/Qualifiers
                                                                                         Contact: Ross Whetten
Forest Biotechnology Group
North Carolina State University
Dept. of Forestry, NC State University, 6113 Jordan Hall, Raleigh
NC, 27695-8008
Tel: 919-515-7800
Fax: 919-515-7801
                                                                                                                                                                                           Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Coniferopsida; Coniferales; Pinaceae; Pinus; Pinus. 1 (bases 1 to 605)
Whetten, R.W., Kinlaw, C.S., Retzel, E. and Sederoff, R.R.
The Pine Gene Discovery Project
Unpublished (1999)
                                                                                                                                                                                                                                                                                                                                                         AW010330 605 bp mRNA linear EST 10-SEI ST04G06 Pine Triplex shoot tip library Pinus taeda cDNA clone ST04G06, mRNA sequence.
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          /(lone_lib="Pine_TriplEx shoot tip library"
//lab_host="E. coli BM25.8"
//lab_host="E. coli BM25.8"
//note="Organ: shoot tips; Vector: Lambda TriplEx; Site_1:
Sfil (A), Site_2: Sfil (B); Shoot tips (approx. 2 cm from apex) were collected during the spring, frozen and used for mRAN isolation. The SMART-PCR method (Clontech) was used to prepare a library from 1 ug total RNA, using the Lambda TriplEx vector. Plasmid subclones in pTriplEx were recovered by cre-lox excision in E. coli strain BM25.8 and sequenced from the 5' end."
s a 119 c 147 g 175 t 9 others
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Dept. of Forest Mycology & Pathology
Swedish University of Agriculture, Box 7026,S-750 07, Uppsala,
                                                                                                                                                                                                                                                                                                                                                                                                                                             143 ATGGGAGTGCATTTACAGTATGGAGTGGTCCAGGTTGTAACAACCGTGCTGAGCGATATA 202
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/db xref="taxon:169015"
/clone="hasp001xd12f"
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Pinus sylvestris/Heterobasidion annosum
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Fax: +46 18 30 92 45
Email: Fred.Asiegbu@mykopat.slu.se
Seq primer: T7 primer:
Location/Qualifiers
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BI416519
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/oreganism="Pinus sylvestris/Heterobasidion annosum"
/db_xref="texcn:169015"
/clone="hasp002xp15f"
/clone="hasp002xp15f"
/clone lib="Heterobasidion annosum - Scots pine infection stage Subtraction cDNA library (hasp)"
/dev_stage="Seedling roots of scots pine were infected for days with H. annosum"
/note="Vector: pT-Adv; Site_1: EcoRI; The subtractive
/note="Vector: pT-Adv; Site_1: EcoRI; The subtractive
hybridization cDNA library was constructed from scots
pine roots infected for 6-days with mycelia of
Heterobasidon annosum (FPS)."
Heterobasidon annosum (FPS)."
24 others
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Eukaryota; mixed EST libraries.

I (bases 1 to 750)
Asiegbu,F.O., Nahalkova,J., Choi,W., Stenlid,J. and Dean,R.A.
Expressed sequence tags of randomly selected cDNA clones from the interaction of the root rot fungus (Hererobasidion annosum) with Unpublished (2001)
6 days with H. annosum" // Incomplete which was a constructed from scots hybridization cDNA library was constructed from scots hybridization for 6-days with mycelia of Heterobasidon annosum (FPS) "
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   436
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Contact: Fred O. Asiegbu
Dept. of Forest Mycology & Pathology
Swedish University of Agriculture, Box 7026,S-750 07, Uppsala,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        257 GCAAATGTGTTGTTCTAATATCGGCAACAACGTTCATGGAGGATACGAGTTCATGTATC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 377 Trrcragcagrerrancaagcrrgcagcagrrrrggraggaagagrrrrrrcarccaar
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   317 AAGGCCAGACTGCTTCTGCTTACAACACGGACAACTGCAAGGGCGTTGCTCAGACCGGT
                                                                                                                                                                                                                                                                                           6
                                                                                                                                                                                                                                Score 88.8; DB 13; Length 726;
Pred. No. 1.4e-14;
                                                                                                                                                                                                                                                                                        92; Indels
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Rax: +46 18 30 92 45
Email: Fred.Asiegbu@mykopat.slu.se
Seg primer: T7 primer.
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BI416967.1 GI:15187990
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Best Local Similarity
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Matches
                                       Query Match
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                   Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GCAAATGTGGGTGTTCTAATATCGGTAACGACGTTCATGGAGGATACGAGTTCGTGTATC 509
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    174;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AW043287 598 bp mRNA linear ST31E09 Pine TriplEx shoot tip library Pinus taeda ST31E09, mRNA sequence.
AW043287
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Forest Biotechnology Group
North Carolina State University
Dept. of Forestry, NC State University, 6113 Jordan Hall, Raleigh
,NC, 27695-8008
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Whetten,R.W., Kinlaw,C.S., Retzel,E. and Sederoff,R.R. The Pine Gene Discovery Project Unpublished (1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Coniferopsida; Coniferales; Pinaceae; Pinus; Pinus.

1 (bases 1 to 598)
                                                                                                                                                                                                                                                                                                                                                                                                                               Email: rosswhet@unity.ncsu.edu
Seq primer: 5' lambda TriplEx2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Contact: Ross Whetten
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Pinus taeda
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                     Similarity
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                                                                                                    146
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         919-515-7800
919-515-7801
    Conservative
                                                                                                                                                          /clone lib="pine TriplEx shoot tip library"
/lab host="E. coli BM25.8"
/note="Organ: shoot tips, Vector: Lambda TriplEx; Site_1:
/note="Organ: shoot tips, Vector: Lambda TriplEx; Site_1:
Sfil (A); Site_2: Sfil (B); Shoot tips (approx. 2 cm from apex) were collected during the spring, frozen and used for mRNA isolation. The SMART-pCR method (Clontech) was used to prepare a library from 1 ug total RNA, using the Lambda TriplEx vector. Plasmid subclones in pTriplEx were
                                                                                                 recovered by cre-lox excision in E. coli strain BM25.8 and sequenced from the 5' end."
3 126 c 150 g 171 t 5 others
                                                                                                                                                                                                                                                                                                                                                     /organism="Pinus taeda"
/db_xref="taxon:3352"
                                                                                                                                                                                                                                                                                                                                                                                                              Location/Qualifiers
                                                                                                                                                                                                                                                                                                                               /clone="ST31E09"
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                 17.4%;
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Pred. No. 9.2e-14;
    0
                     Score 85.6; DB 10;
Pred. No. 1.1e-13;
    Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequencing
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                                         Length 598;
        Indels
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                                                                                             Matches 159;
                                                                                                                 Query Match
Best Local 9
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                                                                                                                                                                                                                 COUNT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            257 CTGGACAAACTGCTGCTCTCTACAACCAGGCTGGATGCAGTGGTGTTGCACACACCAGGT 316
144 AGGGCAGTTATTTCACTGCGTGGGCAGGGCCTGGTTGTAACAACCATGCTGCGCGATACA 203
                                            143 ATGGGAGTGCATTTACAGTATGGAGTGGTCCAGGTTGTAACAACCGTGCTGAGCGATATA 202
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Asiegbu,F.O., Nahalkova,J., Choi,W., Stenlid,J. and Dean,R.A.
Asiegbu,F.O., Nahalkova,J., Choi,W., Stenlid,J. and Dean,R.A.
Expressed sequence tags of randomly selected cDNA clones from the
interaction of the root rot fungus (Heterobasidion annosum) with
seedling roots of Scots pine (Pinus sylvestris)
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Dept. of Forest Mycology & Pathology
Swedish University of Agriculture, Box 7026,8-750
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Unpublished (2001)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Email: Fred.Asiegbu@mykopat.slu.se
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                                                                                                                         Similarity
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                                                                                                Conservative
                                                                                                                                                                                                                                /dev_stages"Seedling roots of scots pine were infected for 6 days with H. annosum"

/notes"Vector: PT-Adv; Site 1: EcoRI; The subtractive hybridization cDNA library was constructed from scots pine roots infected for 6-days with mycelia of Heterobasidon annosum (FPS)."
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stage Subtraction cDNA library (hasp)"
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/db_xref="taxon:169015"
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                                                                                                                      17.2%;
                                                                                                0; Mismatches
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Pred. No. 1.7e-13;
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/clone lib="Heterobasidion annosum - Scots pine infection
stage subtraction cDMA library (hasp)" exert infected for
/dev_stage="Seedling roots of scots pine were infected for
/dev_stage="Seedling roots of scots pine were infected for
/ ays stage="Seedling roots of scots pine were infected for
/ note="Vector: pT-Adv; Site_1: EcoRI; The subtractive
hybridization cDNA library was constructed from scots
pine roots infected for 6-days with mycelia of
letterobasidon annosum (FFS)."
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204 GCAAATGTGGGTGTTCTAATATCGGCAACATTCATGGAGGATACGAGTTCATGTATC 263
                                                                                                      264 AAGGCCAGACCCCTGCGGCTTACAACACGGACAACTGCAAGGGCGTTGCTCAGACCCGGT 323
                                                                                                                                                317 TIGGGTCCAGTGCCA---GGGCATGCAACCCTTTTGGTTGGAAGAGTATCTTCATCCAAT 373
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Contact: Fred O. Asiegbu
Dept. of Forest Mycology & Pathology
Swedish University of Agriculture, Box 7026,S-750 07, Uppsala,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               141 AGGCAGTTATTTCACTGCGTGGGCAGGCCTGGTTGCAACAACCATGCTGCTCGATACA 200
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/db_xref="taxon:169015"
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65.2%; Pred. No. 2.4e-13;
tive 0; Mismatches 76; Indels 9;
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Eukaryota, mixed EST libraries.
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146 18 67 15 98
Fax: +46 18 30 92 45
Email: Fred.Asiegbu@mykopat.slu.se
Seq primer: T7 primer.
Location/Qualifiers
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/clone="haspOtzdo4f"
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stage subtraction CDNA library (hasp)"
6 days with H. annosum"
/note="Wector: pT-Adv; Site_1: EcoRI; The subtractive
hybridization cDNA library was constructed from scots
pine roots infected for 6-days with mycelia of
Heterobasidon annosum (FPS)"
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Eukaryota; mixed EST libraries.

I (bases 1 to 631)

Asiegbu,F.O., Nahalkova,J., Choi,W., Stenlid,J. and Dean,R.A.
Expressed sequence tags of randomly selected CDNA clones from the interaction of the root rot fungus (Heterobasidion annosum) with
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                                321 TITCIGGCAGIGCTAATCAAGAITGCAGCGITTIGGITGGAAGAGITTCTICAICCAGI 380
317 TIGGGTCCAGTGCCA---GGGCATGCAACCCTTTTGGTTGGAAGAGTATCTTCATCCAAT 373
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Contact: Fred O. Astegbu
Dept. of Forest Mycology & Pathology
Swedish University of Agriculture, Box 7026,S-750 07, Uppsala,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     143 ATGGGAGTGCATTTACAGTATGGAGTGGTCCAGGTTGTAACAACCGTGCTGAGCGATATA 202
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Fax: +46 18 30 92 45
Email: Fred Asiegbu@mykopat.slu.se
Seq primer: T7 primer.
Location/Qualifiers
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les 159; Conservative
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                                                                                                                                                                                         CTGGACAAACTGCTGCTCTACAACCAGGCTGGATGCAGTGGTGTTGCACACACCAGGT 316
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                                                                                                                                                                                                                                                                   GCAAGTGTGGATGCTCAGCTATACATCAGAAGGG-----AGGCTATGACTTCAGCTACA 256
GCTA 304
                                                                           Tel: +46 18 67 15 98
Fax: +46 18 30 92 45
Email: Fred.Asiegbudmykopat.slu.se
Seq primer: T7 primer:
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Dept. of Forest Mycology & Pathology
Swedish University of Agriculture, Box 7026,S-750 07, Uppsala,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Asiegbu, F.O., Nahalkova, J., Choi, W., Stenlid, J. and Dean, R.A. Expressed sequence tags of randomly selected cDNA clones from the interaction of the root rot fungus (Heterobasidion annosum) with seedling roots of Scots pine (Pinus sylvestris)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                199
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                stage Bubtraction cDNA library (hasp) "
(dev stage="Seedling roots of scots pine were infected for 6 days with H. annosum"
/note="Vector: pF-Adv; Site 1: EcoRI; The subtractive hybridization cDNA library was constructed from scots pine roots infected for 6-days with mycelia of Heterobasidon annosum (FP5)."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /clone="hasp002xg03f"
/clone_lib="Heterobasidion annosum -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           organism="Pinus sylvestris/Heterobasidion annosum"
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65.2%;
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Pred. No. 2.5e-13;
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RESULT 9 BI416901

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                                                           BI416868 530 bp mRNA linear EST 15-AUG-2001 hasp002xj06f Heterobasidion annosum - Scots pine infection stage subtraction cDNA library (hasp) Pinus sylvestris/Heterobasidion annosum cDNA clone hasp002xj06f, mRNA sequence.
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Fax: +46 18 30 92 45
Email: Fred.Asiegbu@mykopat.slu.
Seq primer: T7 primer.
Seq primer: T7 primer.
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Asiegbu,F.O., Nahalkova,J., Choi,W., Stenlid,J. and Dean,R.A.
Expressed sequence tags of randomly selected cDNA clones from the
interaction of the root rot fungus (Heterobasidion annosum) with
seedling roots of Scots pine (Pinus sylvestris)
Unpublished (2001)
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Dept. of Forest Mycology & Pathology
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Pred. No. 2.6e-13;
D; Mismatches 76;
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/note="Vector: pT-Adv; Site 1: EcoRI; The subtractive hybridization cDNA library was constructed from scots pine roots infected for 6-days with mycelia of Heterobasidon annosum (FPS)."
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    Pinus sylvestris/Heterobasidion annosum.
Pinus sylvestris/Heterobasidion annosum
Eukaryocis, mixed EST libraries.
1 (bases 1 to 510)
Asiegbu, F.O., Nahalkova, J., Choi, W., Stenlid, J. and Dean, R.A.
Expressed sequence tags of randomly selected cDNA clones from the interaction of the root rot fungus (Heterobasidion annosum) with seedling roots of Scots pine (Pinus sylvestris)
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                                                                                                                                                                                                       Contact: Fred Co. Asiegbu
Dept. of Forest Mycology & Pathology
Swedish University of Agriculture, Box 7026,S-750 07, Uppsala,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   143 ATGGGAGTGCATTTACAGTATGGAGTGGTCCAGGTTGTAACAACCGTGCTGAGCGATATA 202
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                                                                                                                                                                                                                                                                                                                                                                                                                               /organism="Pinus sylvestris/Heterobasidion annosum"
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1 (bases 1 to 697)
                                                                                                                                                                                                                                                                                            Tel: +46 18 67 15 98
Fax: +46 18 30 92 45
Email: Fred Asiegbu@mykopat.slu.se
Seg primer: T7 primer.
Location/Qualifiers
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/clone="hasp001xx07f"
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/dev_stage="Secoling roots of scots pine were infected for
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/note="Vector: pT-Adv; Site_l: BcoR1; The subtractive
hybridization cDNA library was constructed from scots
pine roots infected for 6-days with mycelia of
Heterobasidon annosum (FPS)."
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haspOlxnO5f Heterobasidion annosum - Scots pine infection stage subtraction cDNA library (hasp) Pinus sylvestris/Heterobasidion annosum cDNA clone haspO01xnO5f, mRNA sequence.
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Pinus sylvestris/Heterobasidion annosum
Eukaryota, mixed EST libraries.

1 (bases 1 to 531)
Asiegbu,F.O., Nahalkova,J., Choi,W., Stenlid,J. and Dean,R.A.
Asiegbu,F.O., Nahalkova,J., Choi,W., Stenlid,J. and Dean,R.A.
asiegbu,F.O., Nahalkova,J., Choi,W., Stenlid,J. and Dean,R.A.
Asiegbu,F.O., Nahalkova,J., Choi,W., Stenlid,J. and Dean,R.A.
Byressed sequence tags of randomly selected cDNA clones from the
interaction of the root rot fungus (Heterobasidion annosum) with
Unpublished (2011)
Contact: Fred O. Asiegbu
Dept. of Forest Mycology & Pathology
Expressed sequence tags of randomly selected cDNA clones from the interaction of the root rot fungus (Heterobasidion annosum) with seedling roots of Scots pine (Pinus sylvestris) Unpublished (2001)
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                                                                                                                                   Contact: Fred O. Aslegbu
Dept. of Forest Mycology & Pathology
Swedish University of Agriculture, Box 7026,S-750 07, Uppsala,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gapa
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/db_xref="taxon:169015"
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                                                                                                                                                                                                                                                                               Tel: +46 18 67 15 98
Fax: +46 18 30 92 45
Email: Fred.Asiegbu@mykopat.slu.se
Seq primer: T primer:
Location/Qualifiers
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                                                                                                    Dept. of Forest Mycology & Pathology

Dept. of Forest Mycology & Pathology

Dept. of Forest Mycology & Pathology
                                                                                                                                                                                        1 (bases 1 to 374)

Asiegbu, F.O., Nahalkova, J., Choi, W., Stenlid, J. and Dean, R.A. Expressed sequence tags of randomly selected cDNA clones from the interaction of the root rot fungus (Heterobasidion annosum) with seedling roots of Scots pine (Pinus sylvestris)
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BI416726.1 GI:15187749
                                                                                                                                                                                                                                                                                                                                                                                                                                              BI416726 374 bp mRNA linear EST 15-AUG-20 hasp002xa22f Heterobasidion annosum - Scots pine infection stage subtraction cDNA library (hasp) Pinus sylvestris/Heterobasidion annosum cDNA clone hasp002xa22f, mRNA sequence.
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Sweden
  Tel: +46 18 67 15 98
Fax: +46 18 30 92 45
Email: Fred.Asiegbu@mykopat.slu.se
Seq primer: T7 primer.
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Email: Fred.Asiegbu@mykopat.slu.
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                                                                                                                                                                               Unpublished (2001)
                                                                                                                                                                                                                                                                                                                    Eukaryota; mixed EST libraries.
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6 days with H. annosum"

7 notes "Vector: pT-Adv; Site 1: EcoRI; The subtractive hybridization cDNA library was constructed from scote pine roots infected for 6-days with mycelia of Heterobasidon annosum (FP5)."
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1. No. 2e-12;
1. No. 78;
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VERSION
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AGGGCAGTTATTTCACTGCGTGGGCAGGGCCTGGTTGTAACAACCATGCTGCGCGATACA 205
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        148;
                                                                                                                                                                                                                                                                                                                                                                                                                     1 (bases 1 to 476)
Asiegbu,F.O., Nahalkova,J., Choi,W., Stenlid,J. and Dean,R.A.
Expressed sequence tags of randomly selected cDNA clones from the
interaction of the root rot fungus (Heterobasidion annosum) with
seedling roots of Scots pine (Pinus sylvestris)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          hasp001xf17f Heterobasidion annosum - Scots pine infection stage subtraction cDNA library (hasp) Pinus sylvestris/Heterobasidion annosum cDNA clone hasp001xf17f, mRNA sequence.
                                                                                                                                                                                                                     Tal: +46 18 67 15 98
Fax: +46 18 30 92 45
Email: Fred 30 92 45
Email: Fred Asiegbu@mykopat.slu.se
Seq primer: T7 primer.
                                                                                                                                                                                                                                                                                                                                    Contact: Fred O. Asiegbu
Dept. of Forest Mycology & Pathology
Swedish University of Agriculture, Bu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Pinus sylvestris/Heterobasidion annosum Eukaryota; mixed EST libraries.
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104 g 102 t
                    stage subtraction cDNA library (hasp)
/dev_stage="Seedling roots of scots p
6 days with H. annosum"
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/dev_stage="Seedling roots - "
                                                                                 /organism="Pinus sylvestris/Heterobasidion annosum"
/db_xref="taxon:169015"
/clone="hasp001xf17f"
/clone_11b="Heterobasidion annosum - Scots pine inf
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/clone_lib="Heterobasidion annosum -
                                                                                                                                                                                                Location/Qualifiers
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/note="Vector: pT-Adv; Site_1: EcoRI;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GI:15187581
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Pred. No. 6.2e-11;
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                                                                            Scots pine infection
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                                              were infected for
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/organism="Pinus taeda"
/db xref="taxon:3352"
/clone="St2/ST6ZH06"
/clone="St2/ST6ZH06"
/clone="St2/ST6ZH06"
/lab host="E. coli BM55.8"
/nab host="E. coli BM55.8"
/nab host="E. coli BM55.8"
/nab host="E. coli BM55.8"
/nab shoot tips; Vector: Lambda TriplEx; Site_1:
/nab solation: The Sh Noot tips (approx. 2 cm from apex) were collected during the spring, frozen and used for mRNA isolation. The SMATT-PCR method (Clontech) was used to prepare a library from 1 ug total RNA, using the Lambda TriplEx vector. Plasmid subclones in pTriplEx were recovered by cre-lox exclsion in E. coli strain BM25.8 and sequenced from the 5' end."

10 a 67 c 69 g 77 t 11 others
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                294 bp mRNA linear EST 08-SEP-2000 ST62/ST62H06 Pine TriplEx shoot tip library Pinus taeda cDNA clone ST65/ST62H06, mRNA sequence.
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bukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Coniferopsida, Coniferales, Pinaceae, Pinus, Pinus.
1 (bases 1 to 294)
Whetten, W., Kinlaw, C.S., Retzel, E. and Sederoff, R.R.
The Pine Gene Discovery Project
Unpublished (1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Forest Biocechnology Group
North Carolina State University
Dept. of Forestry, NC State University, 6113 Jordan Hall, Raleigh
7.0, 27695-8008
Fax: 919-515-7801
hybridization cDNA library was constructed from scots pine roots infected for 6-days with mycelia of Heterobasidon annosum (FP5)." I others
                                                                                                                                                                                                                                                                               293 GCAGTGGTGTTGCACACACACGTTTGGGTCCAGTGCCAGG---GCATGCAACCCTTTTG 349
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Э
                                                                                                                                              11.6%; Score 57.4; DB 13; Length 476; 66.7%; Pred. No. 1.3e-05; tive 0; Mismatches 46; Indels 3;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Email: rosswhet@unity.ncsu.edu
Seg primer: 5' lambda TriplEx2 Seguencing Primer.
Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                          350 GTTGGAAGAGTATCTTCATCCAATGCT 376
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